Network Systems Science & Advanced Computing

Biocomplexity Institute & Initiative

University of Virginia

Estimation of COVID-19 Impact in Virginia

April 21st, 2021

(data current to April 19th – April 20th)

Biocomplexity Institute Technical report: TR 2021-045

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biocomplexity.virginia.edu

About Us

- Biocomplexity Institute at the University of Virginia
  - Using big data and simulations to understand massively interactive systems and solve societal problems
- Over 20 years of crafting and analyzing infectious disease models
  - Pandemic response for Influenza, Ebola, Zika, and others

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Overview

- **Goal**: Understand impact of COVID-19 mitigations in Virginia
- **Approach:**
  - Calibrate explanatory mechanistic model to observed cases
  - Project based on scenarios for next 4 months
  - Consider a range of possible mitigation effects in "what-if" scenarios
- **Outcomes:**
  - Ill, Confirmed, Hospitalized, ICU, Ventilated, Death
  - Geographic spread over time, case counts, healthcare burdens

Key Takeaways

Projecting future cases precisely is impossible and unnecessary.
Even without perfect projections, we can confidently draw conclusions:

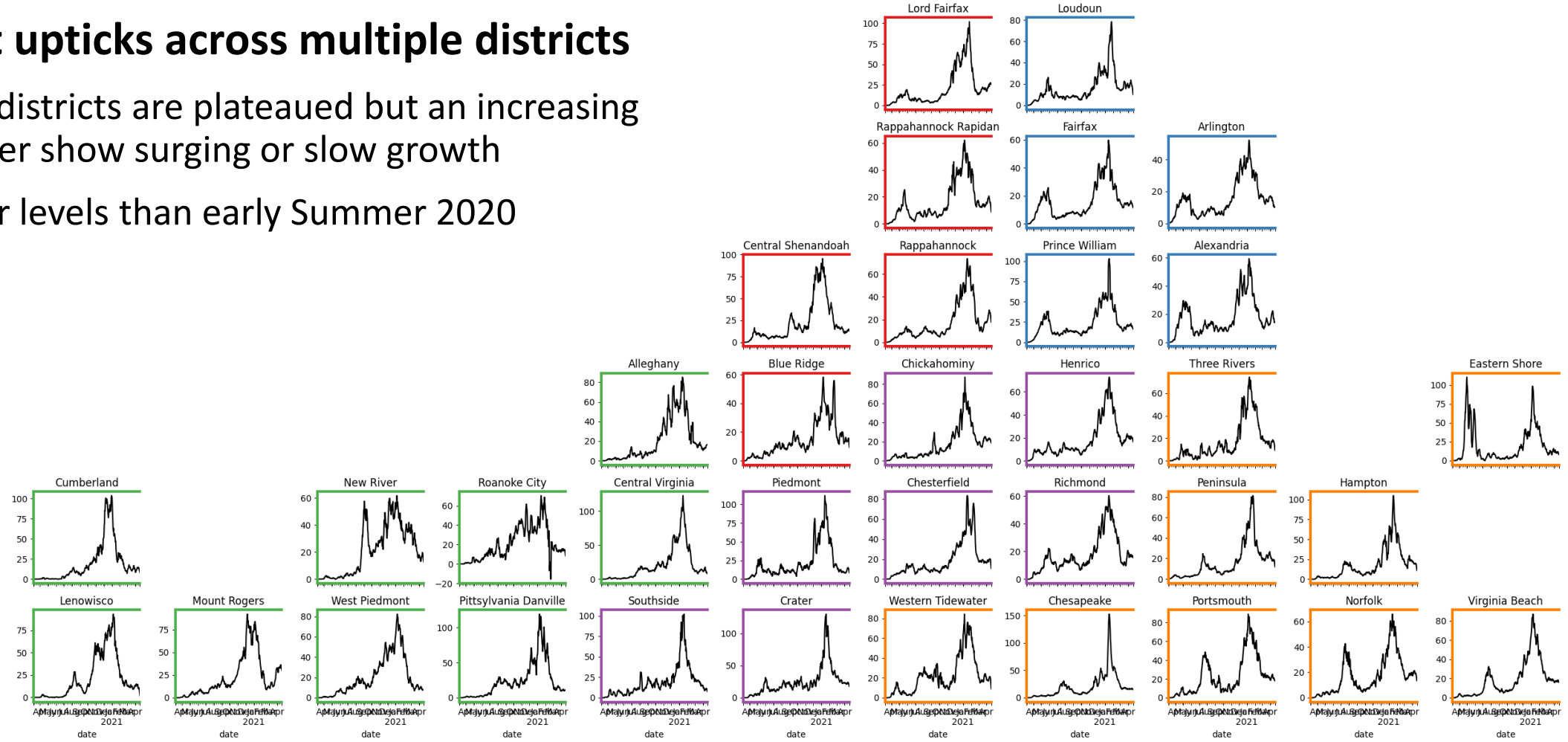
- **Case rates in Virginia have flattened with mix of growth and decline across districts**
- VA mean weekly incidence down to 16/100K from 19/100K, US flat (19 from 19 per 100K)
- Progress remains stalled but is consistent with controls holding their ground despite boosting from B.1.1.7
- Projections show minimal growth overall across Commonwealth, boosted by B.1.1.7, but curtailed by vaccine
- Recent updates:
  - Updated estimates of regional vaccine hesitancy and folded into projections
  - Modeled age-specific vaccinations past and future as well as severity of B.1.1.7 to drive outcome projections
    - Hospitalizations and deaths **reduced** by vaccination in ages most at risk for severe outcomes, but **increased** by prevalence of B.1.1.7
- The situation continues to change. Models continue to be updated regularly.

Situation Assessment

Case Rate (per 100k) by VDH District

Recent upticks across multiple districts

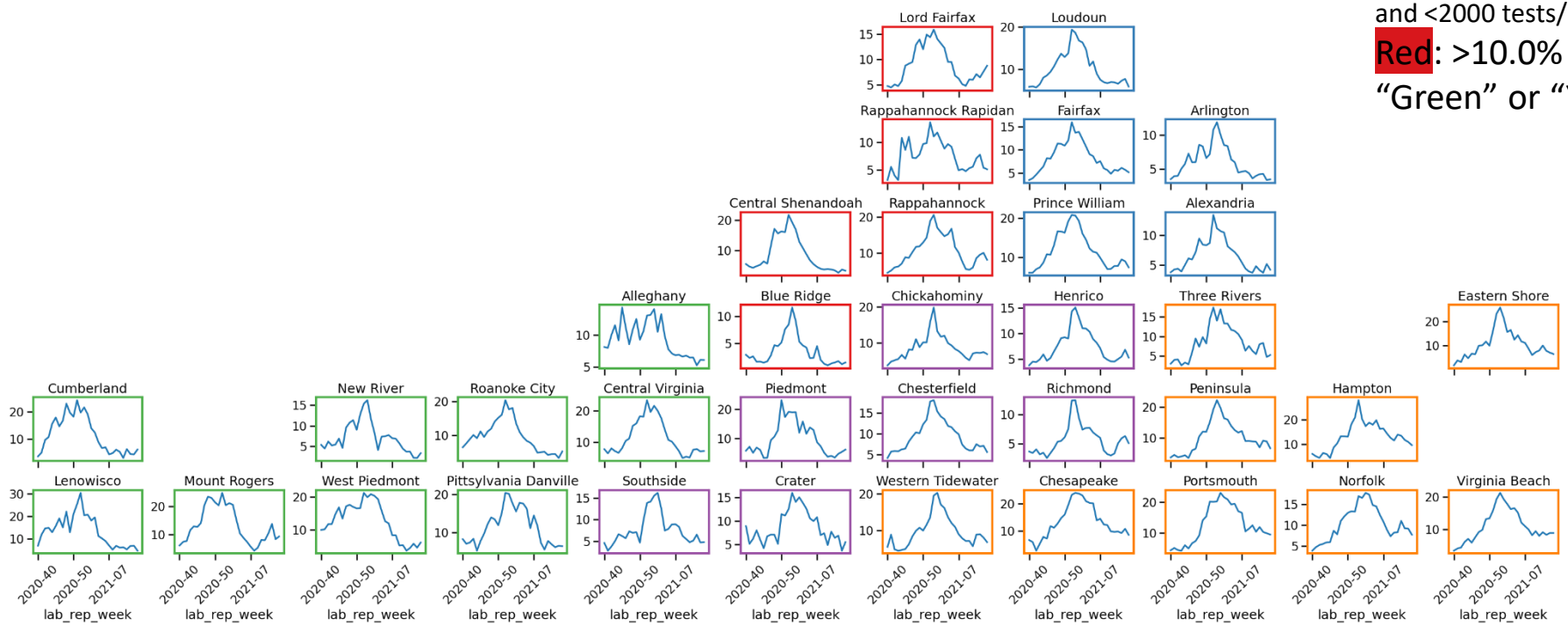
- Most districts are plateaued but an increasing number show surging or slow growth
- Higher levels than early Summer 2020



Test Positivity by VDH District

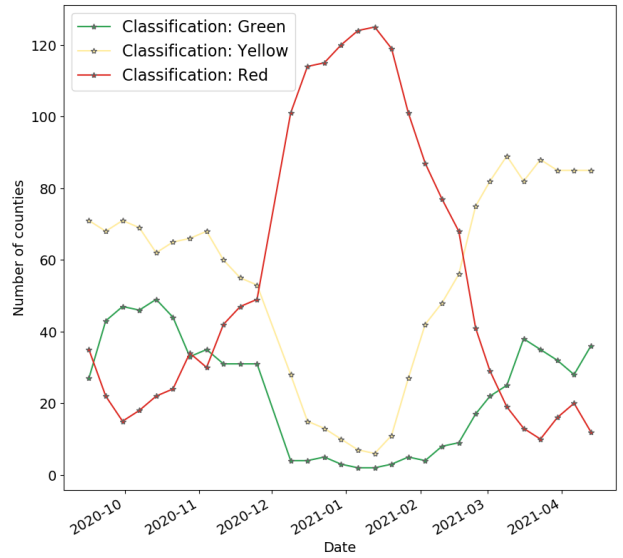
Weekly changes in test positivity by district

- Some upticks/flattening in the positivity rates
- Nearly 75% of counties still in Red or Yellow categories



County level test positivity rates for RT-PCR tests.

Green: Test positivity <5.0%
(or with <20 tests in past 14 days)
Yellow: Test positivity 5.0%-10.0% (or with <500 tests and <2000 tests/100k and >10% positivity over 14 days)
Red: >10.0% and not meeting the criteria for "Green" or "Yellow"



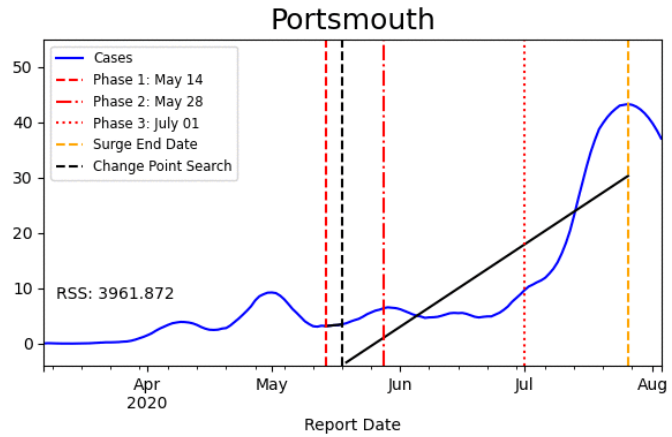
https://data.cms.gov/stories/s/q5r5-gjyu

District Trajectories

Goal: Define epochs of a Health District's COVID-19 incidence to characterize the current trajectory

Method: Find recent peak and use hockey stick fit to find inflection point afterwards, then use this period's slope to define the trajectory

Hockey stick fit

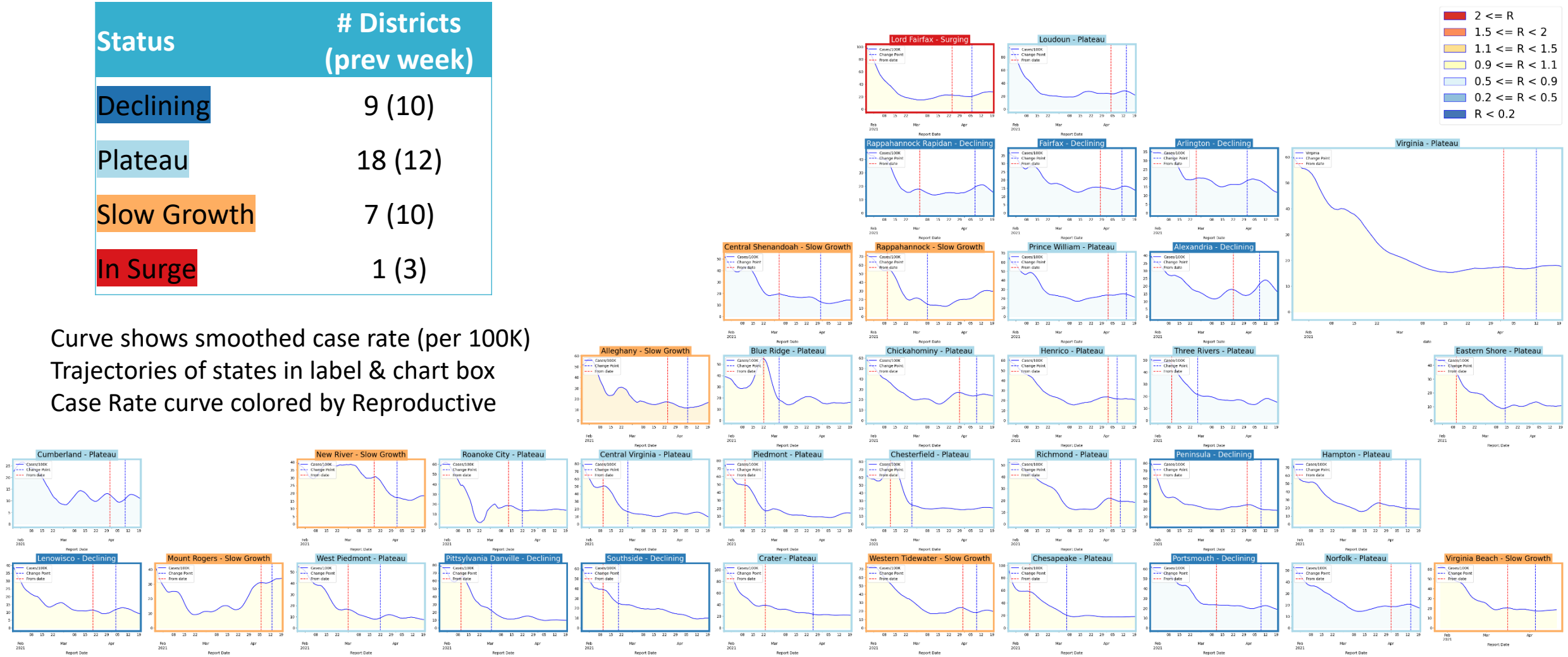


Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	9 (10)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	18 (12)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	7 (10)
In Surge	Currently experiencing sustained rapid and significant growth	2.5 or greater	1 (3)

District Trajectories – last 10 weeks

Status	# Districts (prev week)
Declining	9 (10)
Plateau	18 (12)
Slow Growth	7 (10)
In Surge	1 (3)

Curve shows smoothed case rate (per 100K)
Trajectories of states in label & chart box
Case Rate curve colored by Reproductive



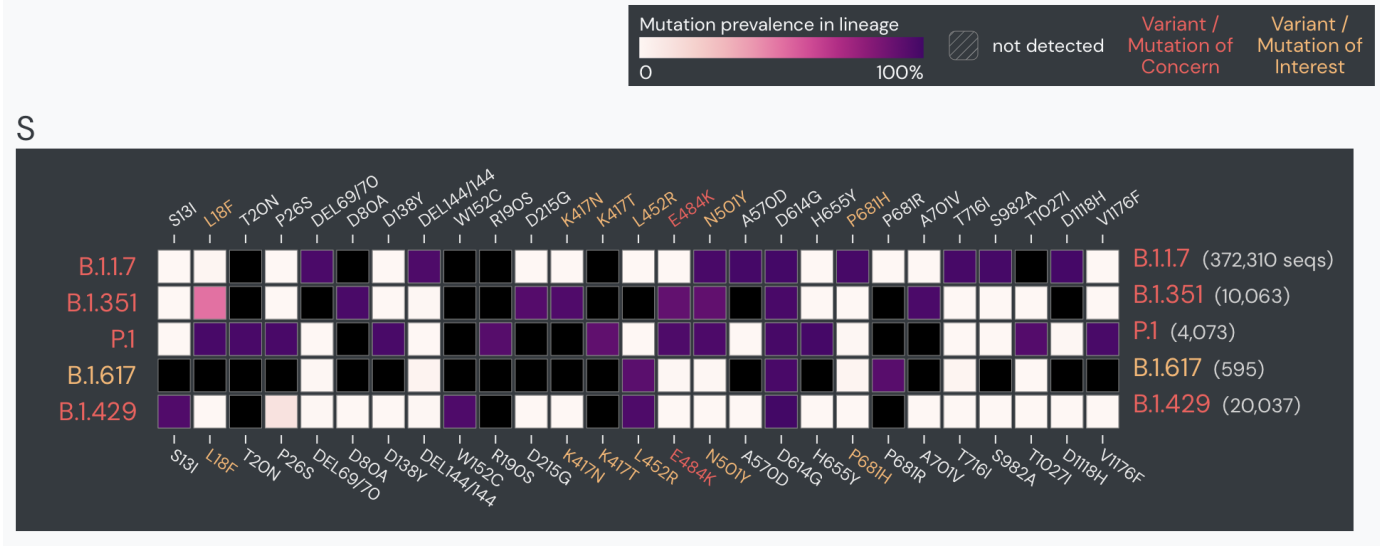
SARS-CoV2 Variants of Concern

Emerging new variants will alter the future trajectories of pandemic and have implications for future control

- Current evidence supports that new variants can:
  - Increase transmissibility
  - Increase severity (more hospitalizations and/or deaths)
  - Limit immunity provided by prior infection and vaccinations
- Genomic surveillance remains very limited
  - Challenges ability to estimate impact in US to date and estimation of arrival and potential impact in future

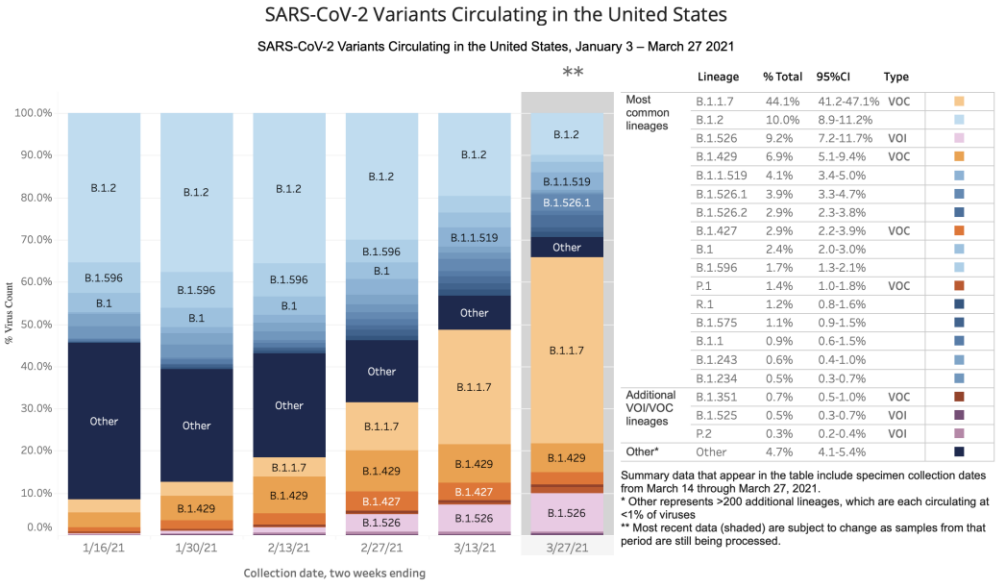
Lineages Of Concern

LoC name	PANGO lineage	NextStrain lineage	Other synonyms	Emergence date	Emergence location	Key AA substitutions in spike protein	Impact
B.1.1.7	B.1.1.7	20I/501Y.V1	VOC 202012/01, UK variant	September 2020	Southeast England	H69-, V70-, N501Y, D614G, P681H	Increased transmissibility; S gene target failure (SGTF)
B.1.351	B.1.351	20H/501Y.V2	South African variant	October 2020	Nelson Mandela Bay, South African	L241-, L242-, A243-, K417N, E484K, N501Y, D614G	loss of serum antibody neutralization
P.1	B.1.1.28	20J/501Y.V3	Brazilian variant	July 2020	Brazil	K417T, E484K, N501Y, D614G	Increased transmissibility; loss of serum antibody neutralization
CAL.20C	B.1.429			July 2020	Southern California, USA	W152C, L452R, D614G	loss of monoclonal antibody binding
B.1.375	B.1.375			September 2020	Massachusetts, USA	H69-, V70-, D614G	S gene target failure (SGTF)



outbreak.info [Outbreak Info](#)

[NIH-NIAID Bacterial-Viral Bioinformatics Resource Center](#)



CDC [CDC Variant Tracking](#)

SARS-CoV2 Variants of Concern

Lineage B.1.1.7

- B.1.1.7 has been detected in Virginia and has continued to rapidly grow though has been hard to track. Current estimates suggest prevalence has exceeded the 50% level in VA and US. Growth rate slowing in some states with high levels.

Transmissibility:

- Science study using two-strain model supports that increased transmissibility, duration of infectiousness, or increased transmission in children best fit the epi data observed in the UK across regions. Some combination of all also likely.
- Study from Public Health England shows contacts of B.1.1.7 cases are more likely (50%) to test positive than contacts of non-B.1.1.7 patients
- Study shows B.1.1.7 patients have longer periods of infection

Severity:

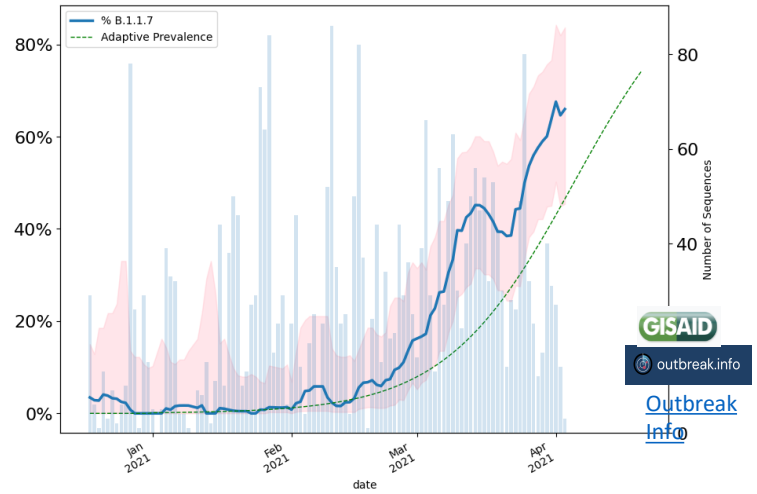
- Evidence continues to mount supporting increased risks of hospitalization and mortality for B.1.1.7 infected individuals
- Danish study shows B.1.1.7 to have a 64% higher risk of hospitalization, while Public Health Scotland studies showed a range of 40% to 60%
- Study in Nature based on UK data estimates B.1.1.7 cases have 60% higher mortality
- Sequence based study of hospitalized patients in Lancet, found no association with severity and death among hospitalized from B.1.1.7

Table 1 | Absolute 28-day mortality risk associated with B.1.1.7, as expressed by case fatality ratio (%) among individuals testing positive in the community

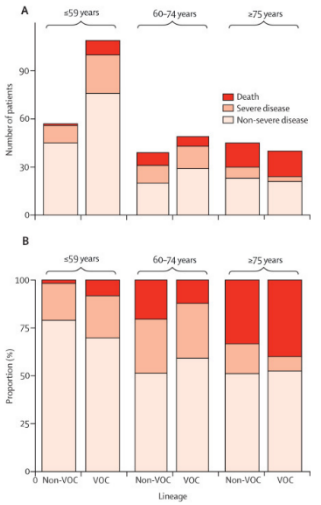
Sex	Age	Baseline	SGTF, complete cases	p_{VOC}, IPW
Female	0–34	0.00069%	0.0011% (0.00096–0.0012%)	0.0011% (0.00097–0.0012%)
	35–54	0.033%	0.050% (0.045–0.056%)	0.052% (0.046–0.059%)
	55–69	0.18%	0.28% (0.25–0.31%)	0.29% (0.26–0.33%)
	70–84	2.9%	4.4% (4.0–4.9%)	4.6% (4.0–5.1%)
	85 and older	13%	19% (17–21%)	20% (18–22%)
Male	0–34	0.0031%	0.0047% (0.0042–0.0052%)	0.0049% (0.0043–0.0055%)
	35–54	0.064%	0.099% (0.089–0.11%)	0.10% (0.090–0.12%)
	55–69	0.56%	0.86% (0.77–0.95%)	0.89% (0.78–1.0%)
	70–84	4.7%	7.2% (6.4–7.9%)	7.4% (6.6–8.3%)
	85 and older	17%	25% (23–27%)	26% (23–29%)

The baseline risk (i.e., for preexisting SARS-CoV-2 variants) is derived using linked deaths within 28 days for all individuals testing positive in the community from 1 August – 31 October 2020. Adjusted risks are presented for the SGTF analysis for complete cases and for the misclassification-adjusted (p_{VOC}) IPW analysis, which yielded the lowest and highest mortality estimates, respectively, of the main models assessed (Fig. 2a–d).

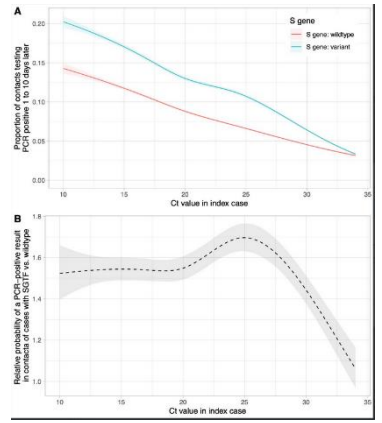
Virginia - 66.0% (B.1.1.7)
Source: outbreak.info



Outbreak Info



Of 496 patients with samples positive for SARS-CoV-2 on PCR and who met inclusion criteria, 341 had samples that could be sequenced. 198 (58%) of 341 had B.1.1.7 infection and 143 (42%) had non-B.1.1.7 infection. We found no evidence of an association between severe disease and death and lineage (B.1.1.7 *vs* non-B.1.1.7) Lancet



PCR testing in England from Sept 2020 – Feb 2021 combined with contact tracing data found B.1.1.7 cases to have higher viral loads (based on PCR cycle thresholds) and increased likelihood of causing infections among contacts. B.1.1.7 increased transmission by ~50%. Medrxiv

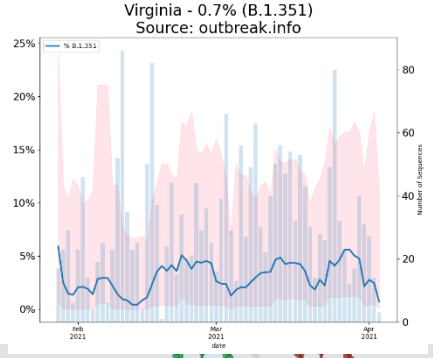
SARS-CoV2 Variants of Concern

Lineage B.1.351

- Emerging strain initially identified in South Africa shows signs of vaccine escape, currently 452 reported cases in 36 states (including 37 now in Virginia)

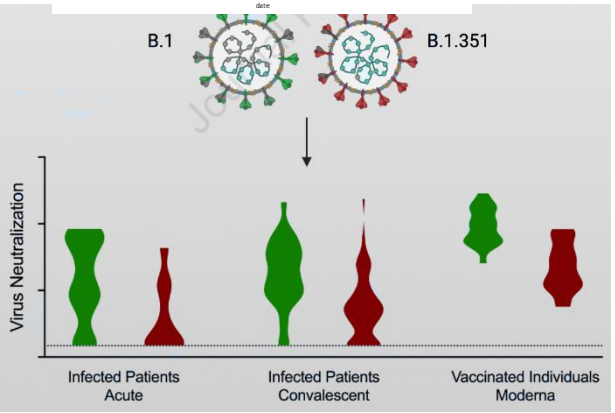
Immune Escape:

- Many studies show that convalescent sera from previously infected individuals does not neutralize B.1.351 virus well, however, vaccine induced immunity shows signs of effectiveness
- One study supports a previous study based on clinical trial data showing that convalescent serum neutralization is highly predictive of actual immune protection for infection
- Another study in Cell supports previous report demonstrating that despite reduced antibody binding, the Moderna vaccinated individuals able to neutralize the B.1.351 variant
- New England Journal Study shows that people with prior infections who are then vaccinated (one dose of Pfizer) the boosted immunity is effective against B.1.351
- Some evidence emerging that variants like B.1.351 may be more likely to cause secondary infections after vaccination. As more of the population is protected we may find B.1.351 and other immune evading variants becoming more prevalent.

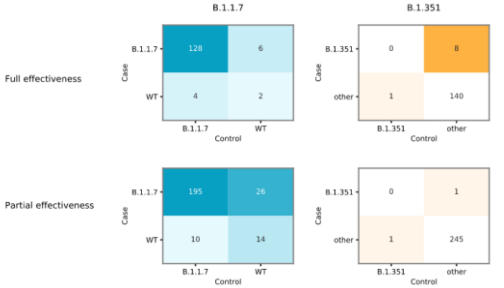


GISAID outbreak.info

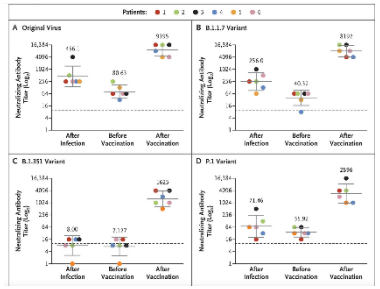
Outbreak Info



Despite reduced antibody binding to the B.1.351 RBD, sera from infected (acute and convalescent) and Moderna (mRNA-1273) vaccinated individuals were still able to neutralize the SARS-CoV-2 B.1.351 variant. Cell



Small Case control study suggests that among those infected after their 1st and 2nd dose, they are more likely to be B.1.351 in the earlier infections, and B.1.1.7 in the later breakthrough infections. Medrxiv

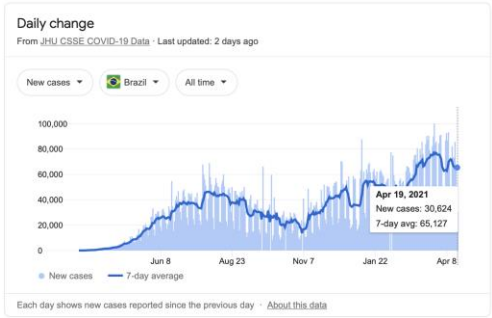


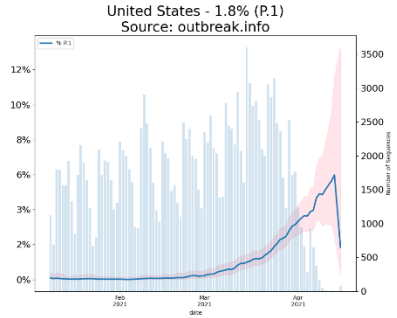
Six patients previously infected with the original virus received the BNT162b2 vaccine. Before vaccination, they had neutralizing activity against the B.1.1.7 and P.1 variants but not B.1.351. After one dose, neutralizing activity against all variants increased greatly. NEJM

SARS-CoV2 Variants of Concern

Lineage P.1

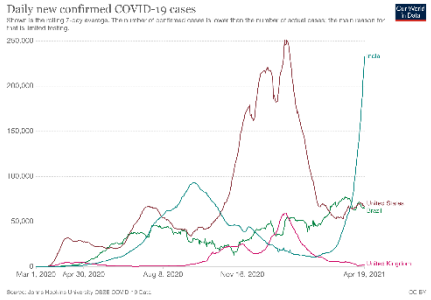
- At least 1.4% prevalence in US, likely higher, while Brazil suffering significant case loads for prolonged period has 43% prevalence
- Study in Cell shows P.1 may be less resistant to neutralization than B.1.351

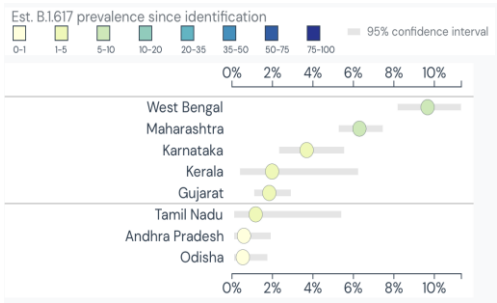




Lineage B.1.617

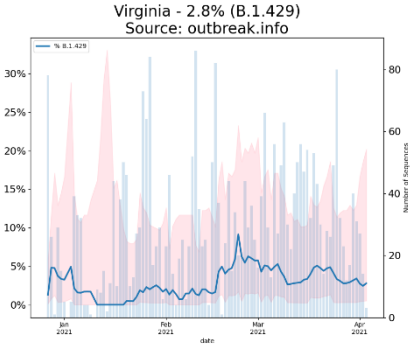
- Suspected of driving significant surge in India, so called “double mutant” mutant possess mutations similar to B.1.1.7, B.1.351, and B.1.429; thus more transmissible and able to partially evade immunity
- A few cases already identified in UK and US as well
- Limited genomic surveillance finds B.1.617 in over 5% of samples in several states, with recent report of over 60% in one set of samples





Lineage B.1.429/427 and B.1.526 and subvariants

- Combined account for over 25% of circulating virus in US
- Evidence suggests these variants as slightly more transmissible and also exhibit some immune escape



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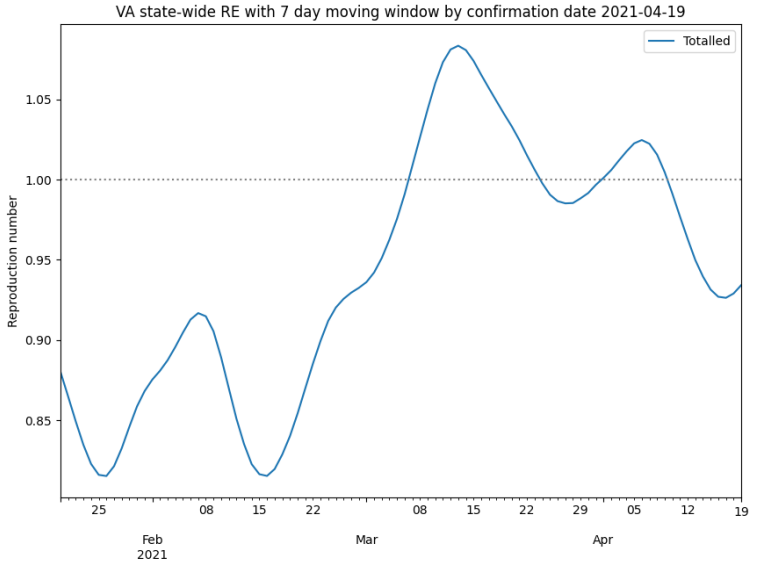
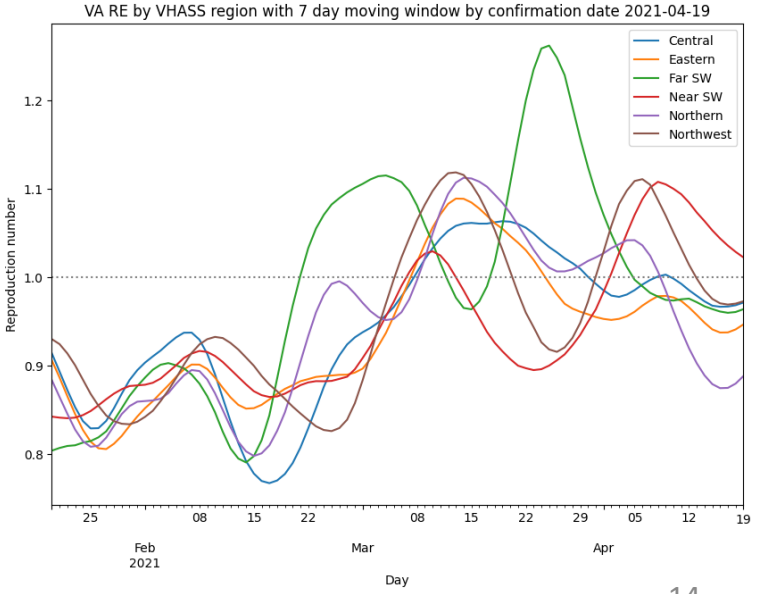
Estimating Daily Reproductive Number

April 19th Estimates

Region	Date Confirmed R_e	Date Confirmed Diff Last Week
State-wide	0.935	-0.074
Central	0.973	0.002
Eastern	0.945	-0.001
Far SW	0.958	0.011
Near SW	1.021	-0.006
Northern	0.889	-0.174
Northwest	0.975	-0.051





Methodology

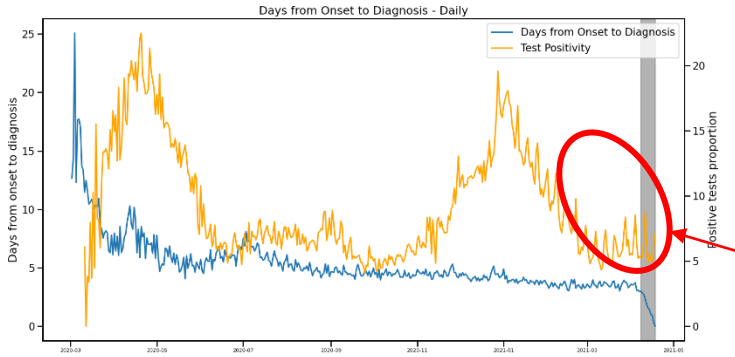
- Wallinga-Teunis method (EpiEstim[1]) for cases by **confirmation date**
- Serial interval: updated to discrete distribution from observations (mean=4.3, Flaxman et al, Nature 2020)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

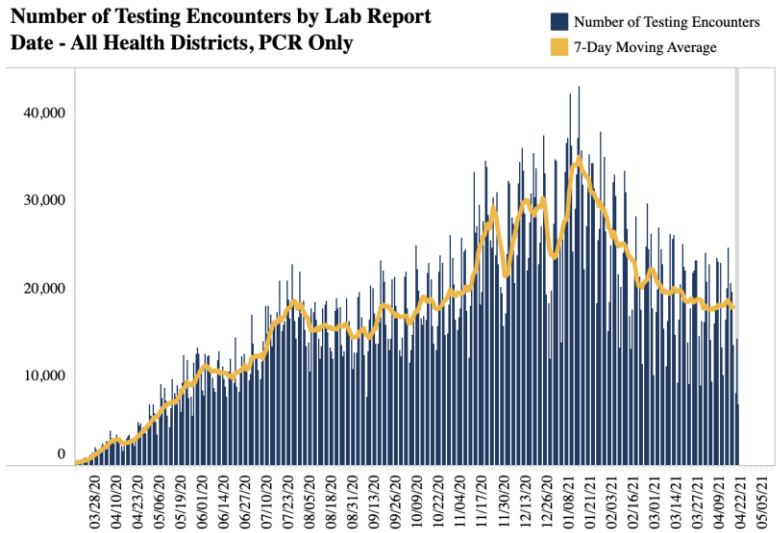
1. Anne Cori, Neil M. Ferguson, Christophe Fraser, Simon Cauchemez. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, Volume 178, Issue 9, 1 November 2013, Pages 1505–1512, https://doi.org/10.1093/aje/kwt133

Changes in Case Detection

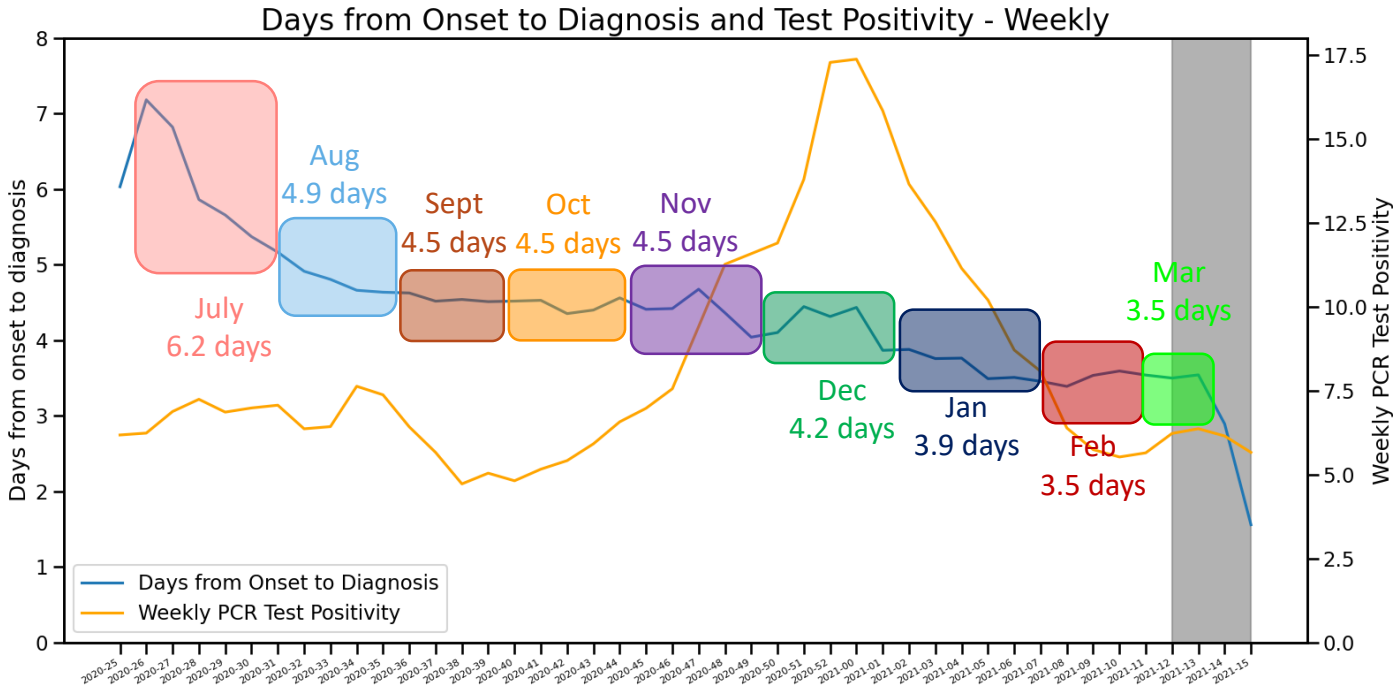
Timeframe (weeks)	Mean days	% difference from overall mean
July (26-30)	6.2	-5%
Aug (31-34)	4.9	-25%
Sept (35-38)	4.6	-29%
Oct (39-43)	4.5	-31%
Nov (44-47)	4.5	-30%
Dec (48-49)	4.3	-35%
Jan (00-04)	3.9	-39%
Feb (05-08)	3.5	-47%
Mar (09-13)	3.5	-45%
Overall (13-12)	6.5	--

Test positivity vs. Onset to Diagnosis

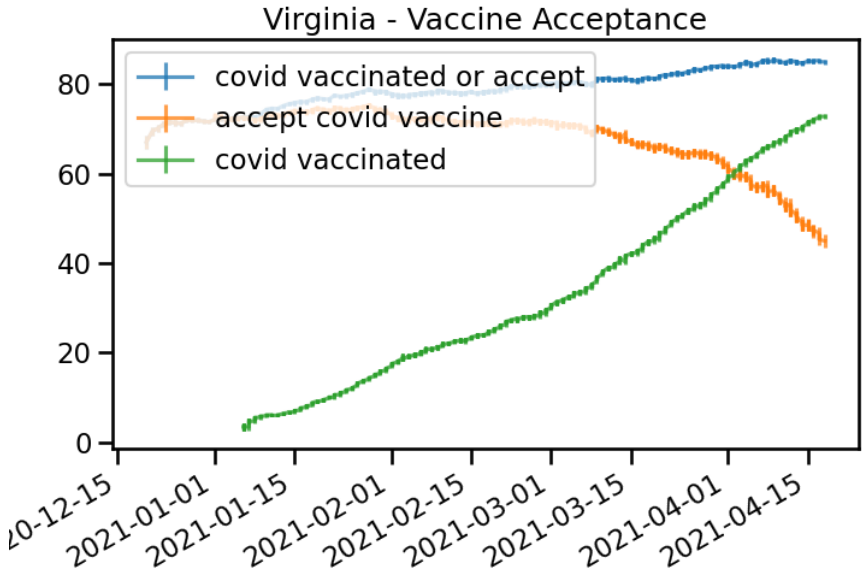


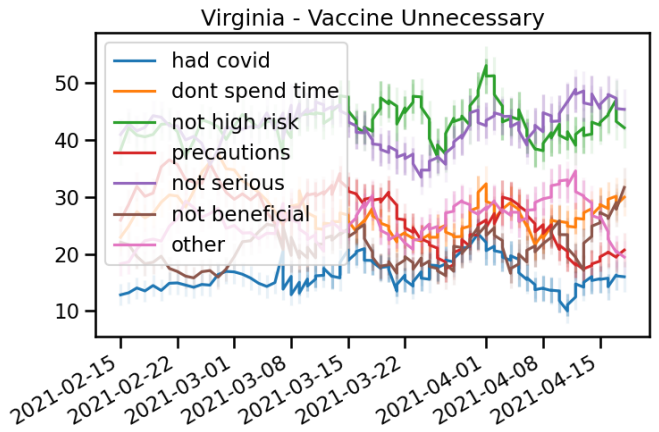


Accessed 9:00am April 21, 2021
https://www.vdh.virginia.gov/coronavirus/



Vaccine Acceptance in Virginia

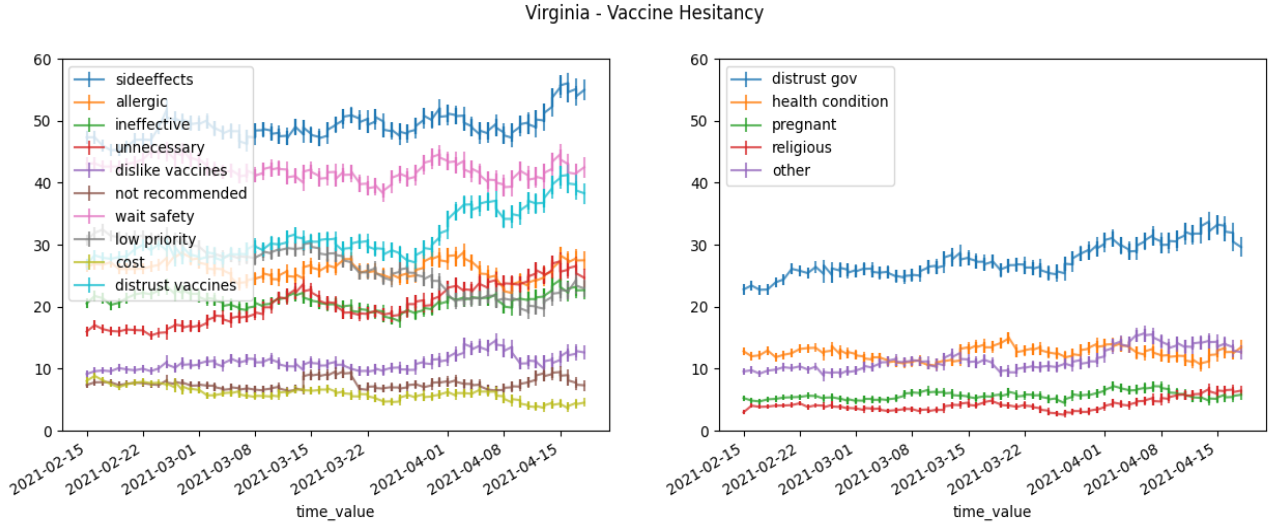




Data Source: https://covidcast.cmu.edu

Acceptance remains high:

- Proportion of Virginians that have already or would definitely or probably accept vaccination if offered today
- *Survey respondents are reporting high levels of vaccination of ~70% reflecting some bias of the mechanism*
- Over 80% of Virginians have already or will choose to be vaccinated
- Top reasons for hesitancy: side effects, safety, distrust (increasing)
- Reasons for unnecessary vaccine: increasing levels of “not serious” disease in past 2 weeks

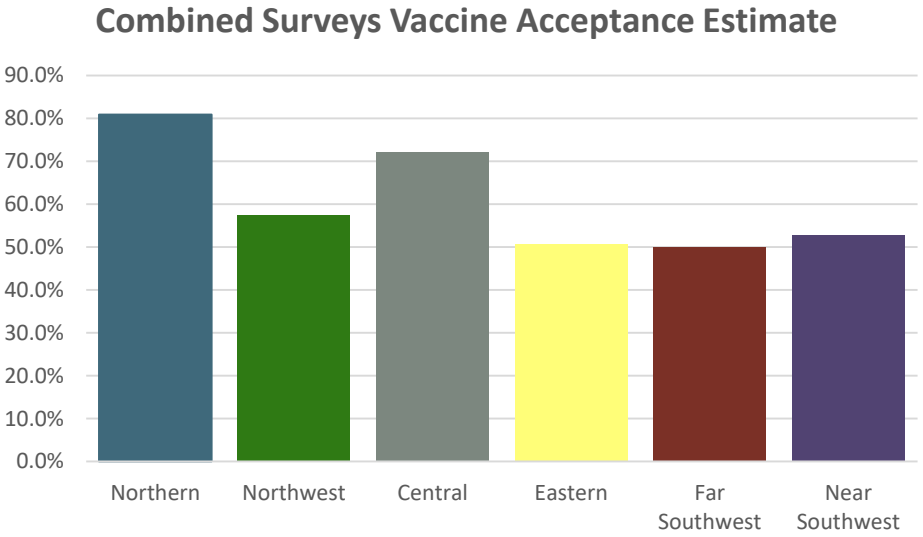


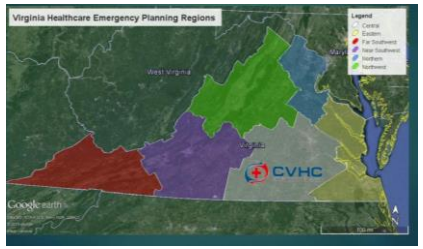
Vaccination Acceptance by Region

Combined Surveys:

- Facebook administered survey is timely and broad, but biased by who accesses Facebook and answers the survey
- Traditional phone-based survey administered several weeks ago for VDH vaccine messaging purposes is better sampled for true representativeness
- Correction approach:
  - Calculate an over-reporting fraction based on number reporting being vaccinated (Apr 8-14) vs. VDH administration data
  - Cross-validate coarse corrections against traditional survey
  - Values were similar across regions, except in Eastern and Northwest which had more than 10% difference. We took a mean of the two surveys to create a coarse estimate.

Virginia Region	Vaccinated Already or Accepting of Vaccine
Northern	81%
Northwest	57%
Central	72%
Eastern	51%
Far Southwest	50%
Near Southwest	53%





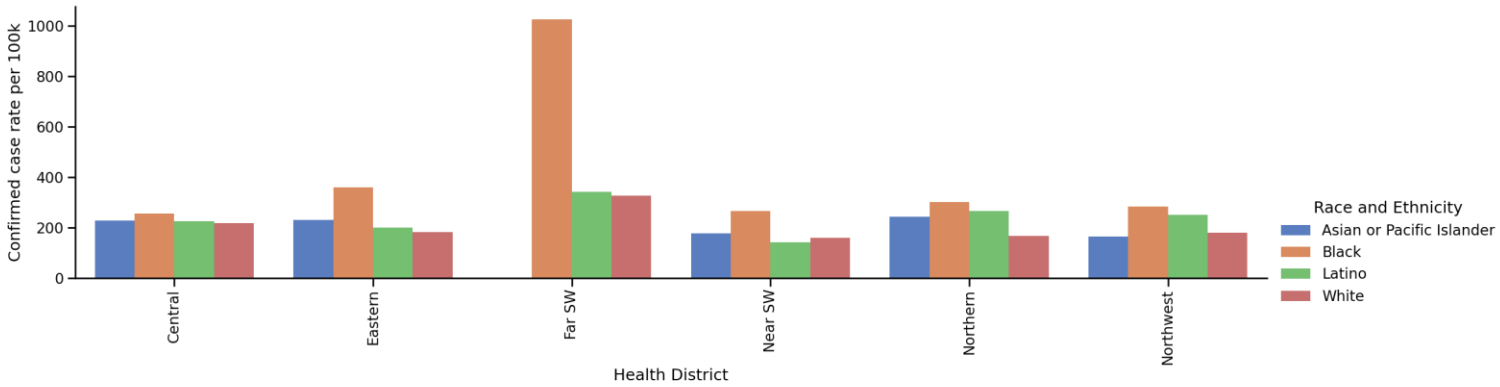
Data Source: https://covidcast.cmu.edu

Race and Ethnicity – Recent Rate Changes (per 100K)

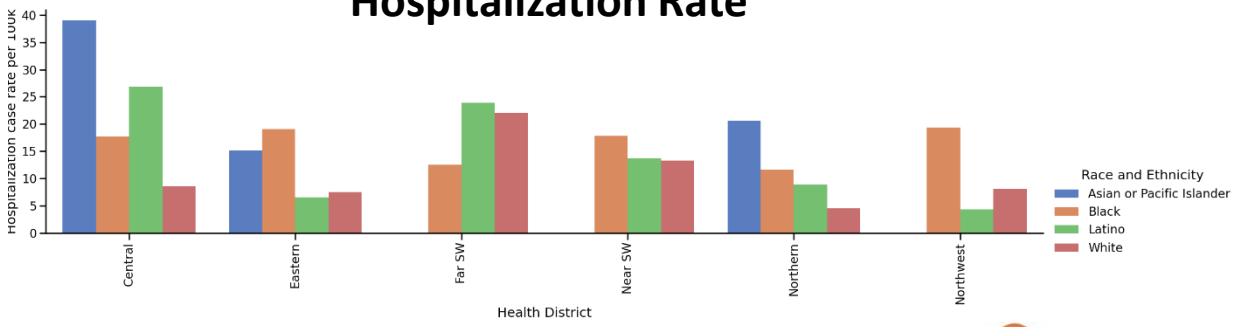
Changes in Race and Ethnicity Rates (per 100k) in past two weeks

- Two week change in population level rates
- Black, Latinx and 2 or more races populations have much higher changes in rates; disparity is more pronounced in some regions than others
- Based on 2019 census race-ethnicity data by county

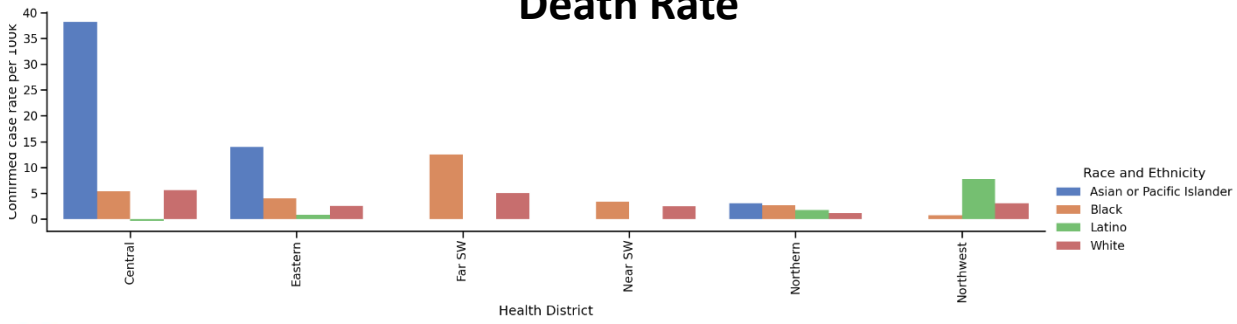
Case Rate



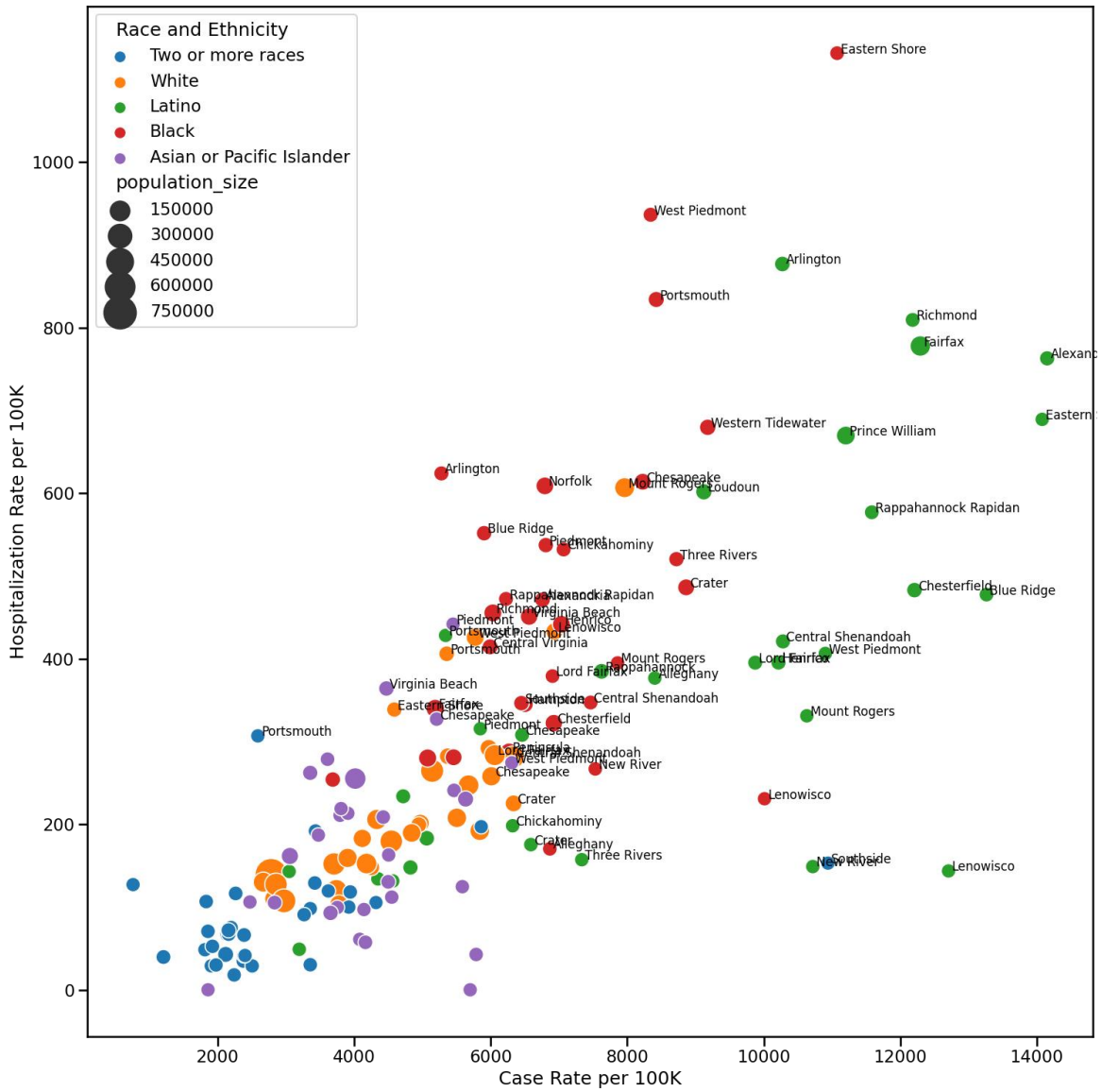
Hospitalization Rate



Death Rate



Race and Ethnicity cases per 100K

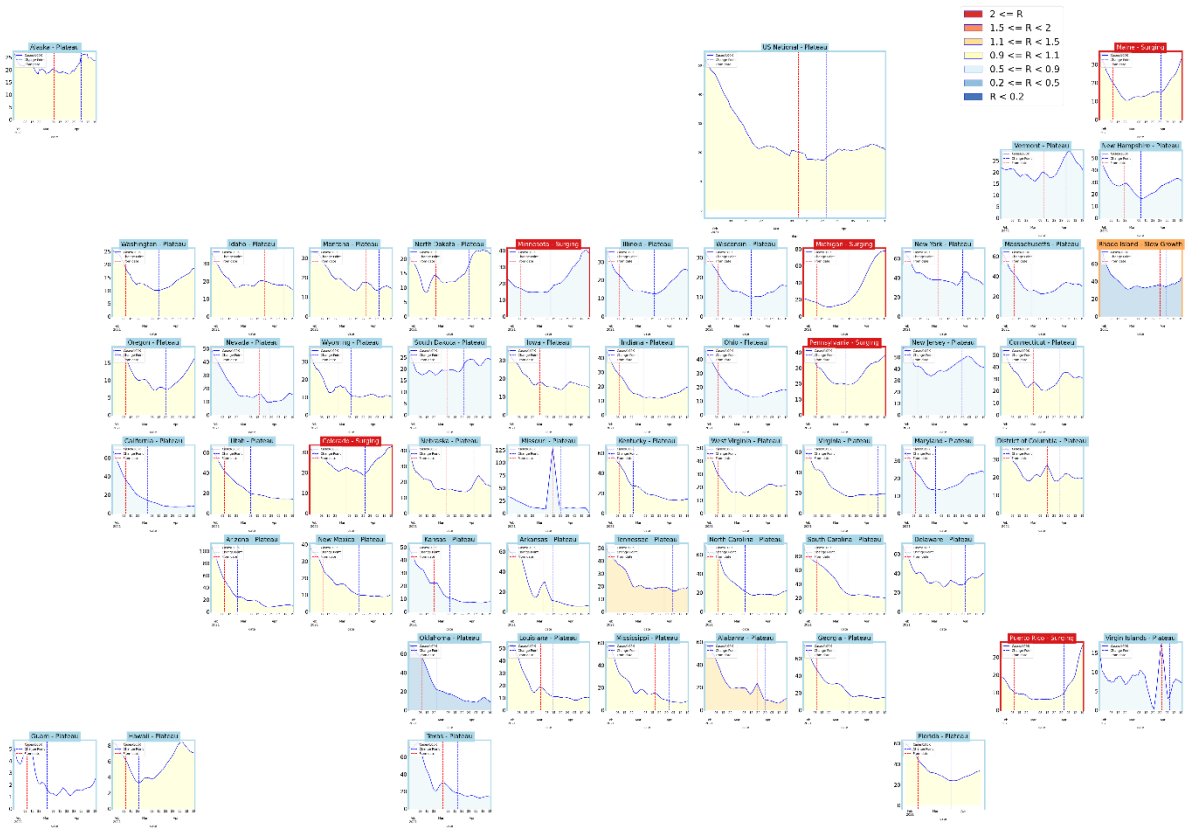


Rates per 100K of each Racial-Ethnic population by Health District

- Each Health District's Racial-Ethnic population is plotted by their Hospitalization and Case Rate
- Points are sized based on their overall population size (overlapping labels removed)

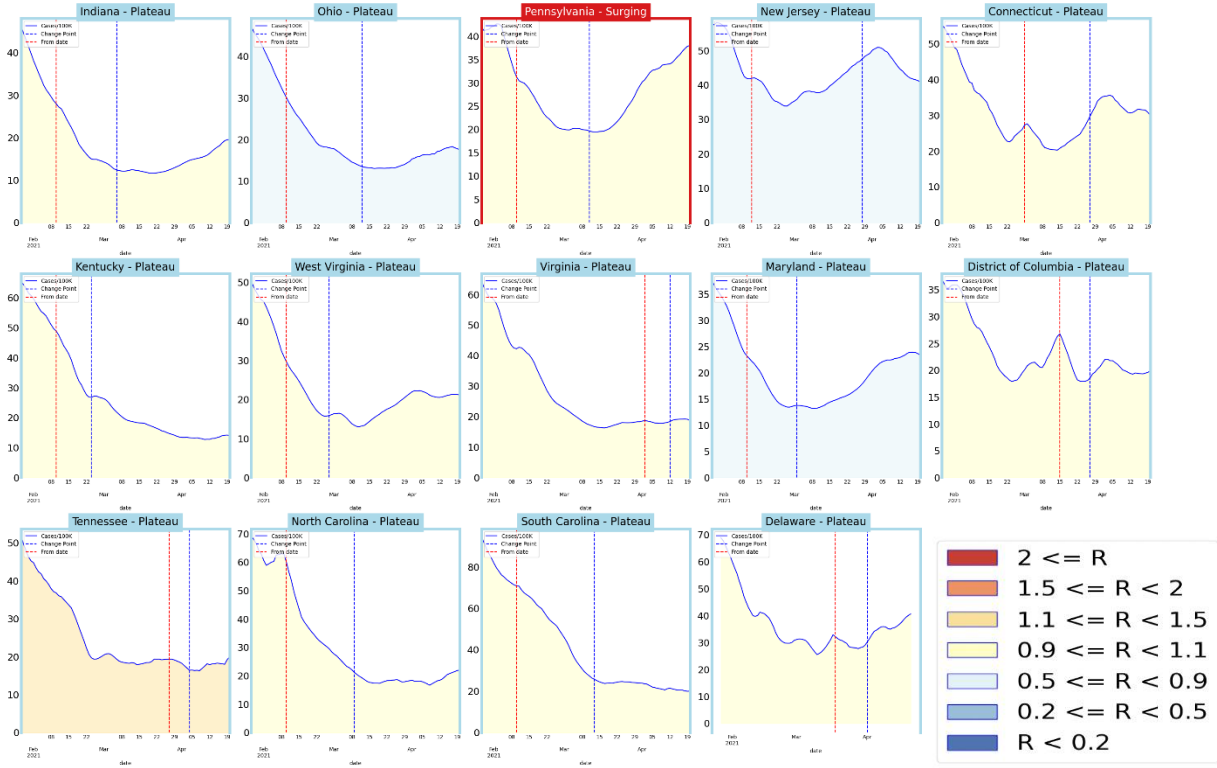
Other State Comparisons

Trajectories of States



- Nearly all states are plateaued, with 6 jurisdictions now in surge, though several are leveling off
- Several states experienced short periods of growth but have since slowed / declined

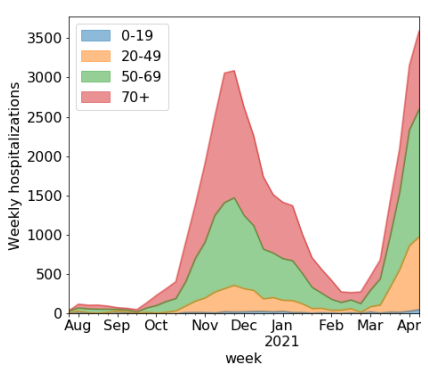
Virginia and her neighbors

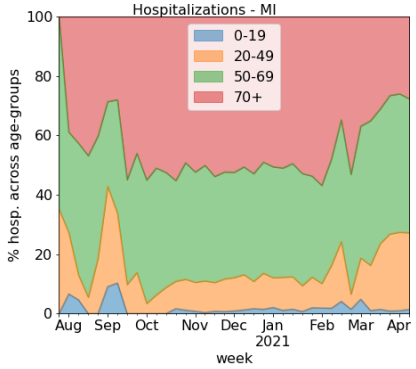


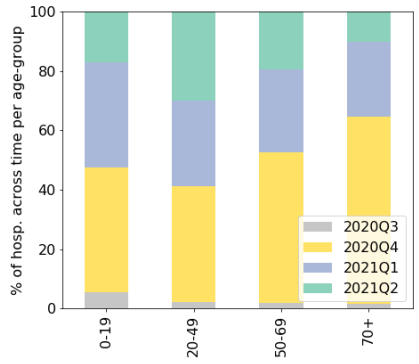
- VA and neighbors are in plateau, with a few to the north showing more growth
- Levels remain high but volatility is low

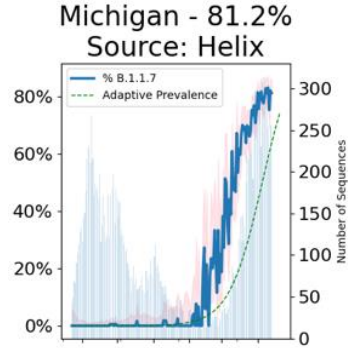
Other State Comparisons - Hospitalizations

Michigan

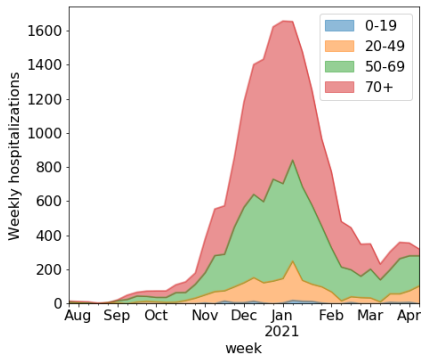


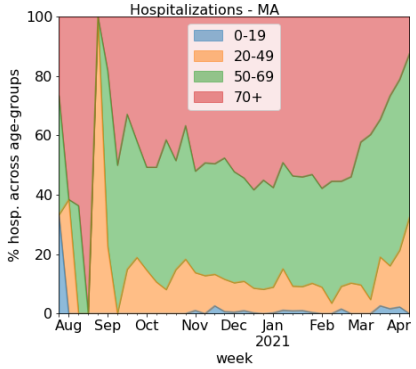


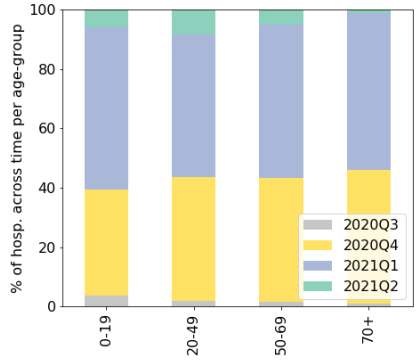


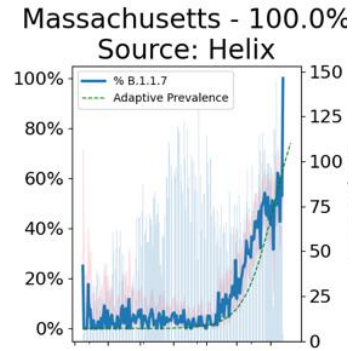


Massachusetts

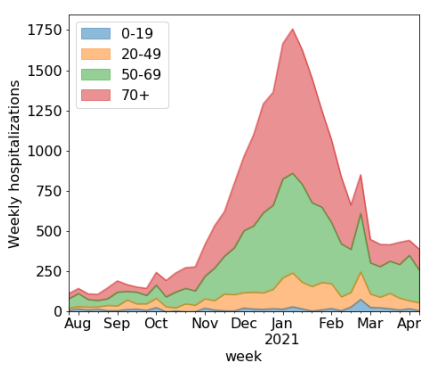


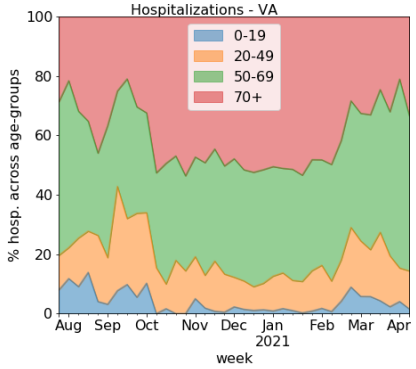


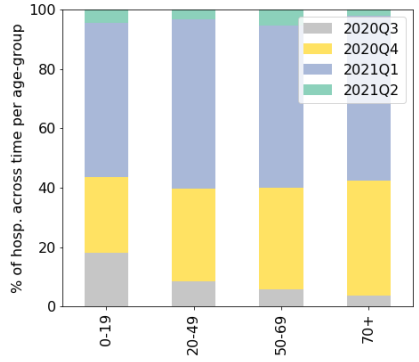


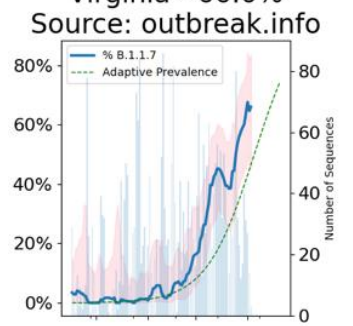


Virginia









Shifting Age Distribution of cases being hospitalized

- Dual forces of vaccinations in older groups and severity of B.1.1.7 are dramatically shifting the age distribution of hospitalized patients
- Michigan's hospitalizations are rising steeply, consist of more 20-59 year olds
- Massachusetts has significant B.1.1.7 prevalence but one of the highest vaccination levels
- Virginia has high vaccination and is maintaining lower levels of hospitalizations

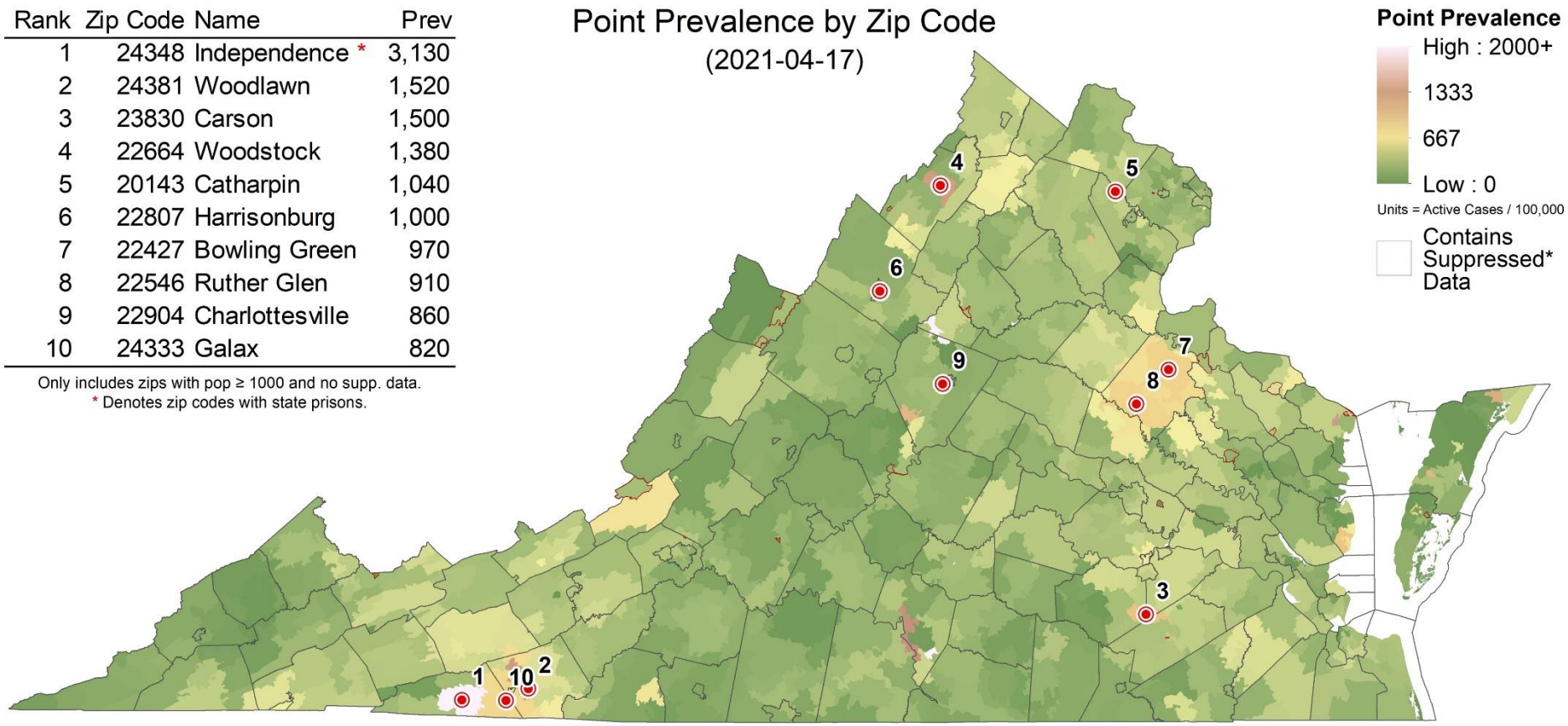
Zip code level weekly Case Rate (per 100K)

Case Rates in the last week by zip code

- Concentrations in Southwest, which was preceded by cluster of increased HCW rates last week
- Still some universities in top 10
- Some counts are low and suppressed to protect anonymity, those are shown in white

Rank	Zip Code	Name	Prev
1	24348	Independence *	3,130
2	24381	Woodlawn	1,520
3	23830	Carson	1,500
4	22664	Woodstock	1,380
5	20143	Catharpin	1,040
6	22807	Harrisonburg	1,000
7	22427	Bowling Green	970
8	22546	Ruther Glen	910
9	22904	Charlottesville	860
10	24333	Galax	820

Only includes zips with pop ≥ 1000 and no supp. data.
* Denotes zip codes with state prisons.



Based on Spatial Empirical Bayes smoothed point prevalence for week ending 2021-04-17.
Note: New color ramp scale and new ascertainment ratio of 2:1.

UNIVERSITY of VIRGINIA
BIOCOMPLEXITY INSTITUTE

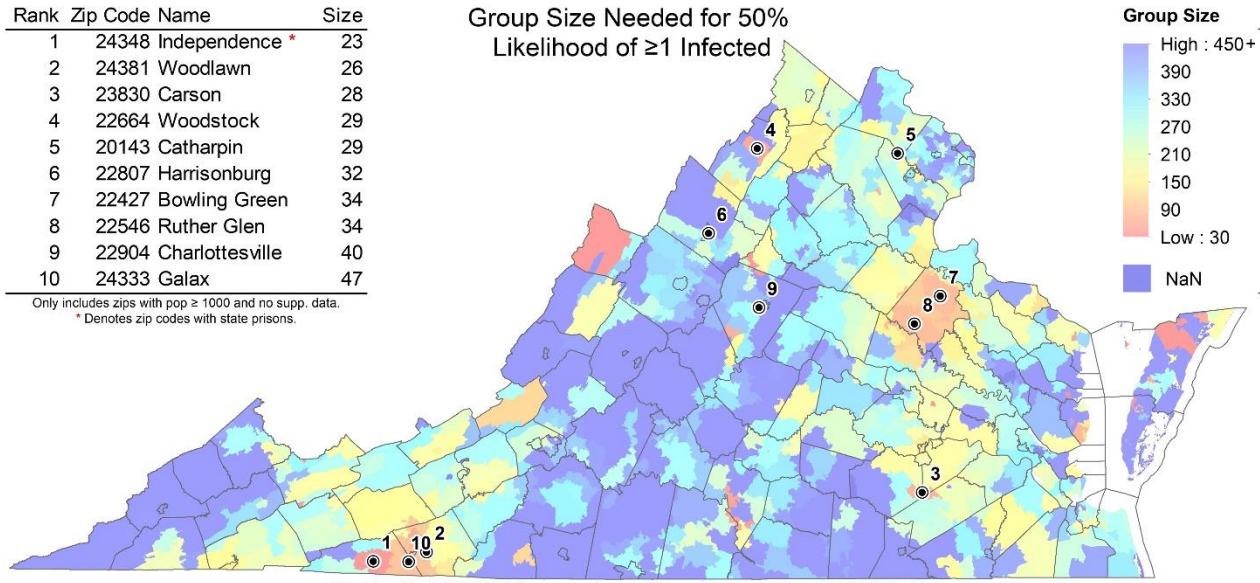
Risk of Exposure by Group Size and HCW prevalence

Case Prevalence in the last week by zip code used to calculate risk of encountering someone infected in a gathering of randomly selected people (group size 25)

- **Group Size**: Assumes 2 undetected infections per confirmed case (ascertainment rate from recent seroprevalence survey), and shows minimum size of a group with a 50% chance an individual is infected by zip code (eg in a group of 23 in Independence, there is a 50% chance someone will be infected)
- **HCW prevalence**: Case rate among health care workers (HCW) in the last week using patient facing health care workers as the denominator

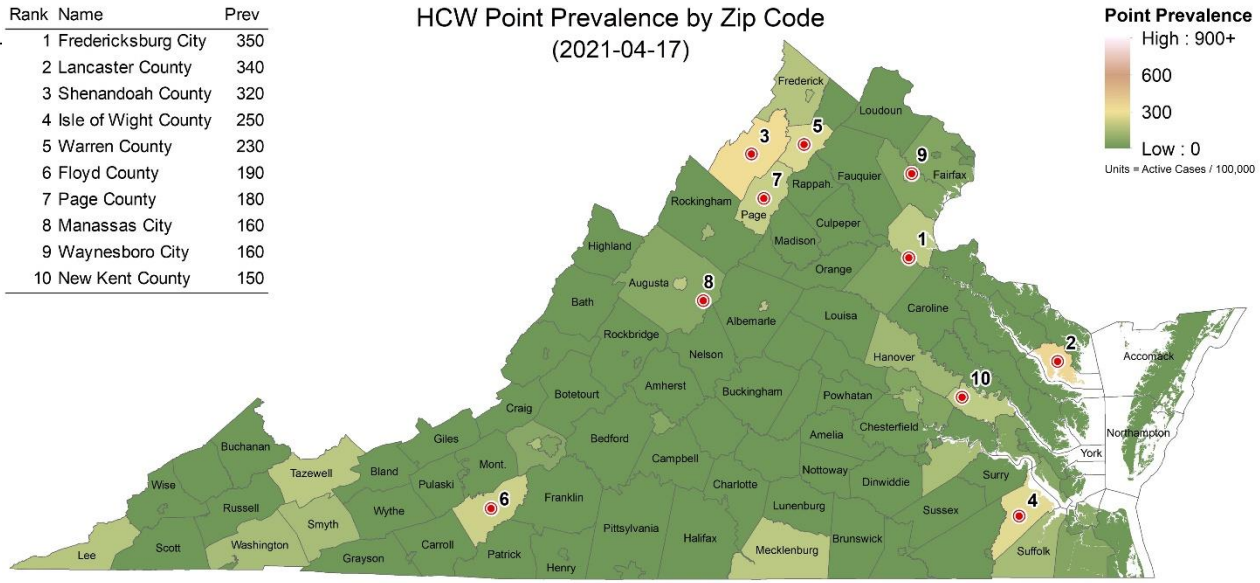
Rank	Zip Code	Name	Size
1	24348	Independence *	23
2	24381	Woodlawn	26
3	23830	Carson	28
4	22664	Woodstock	29
5	20143	Catharpin	29
6	22807	Harrisonburg	32
7	22427	Bowling Green	34
8	22546	Ruther Glen	34
9	22904	Charlottesville	40
10	24333	Galax	47

Only includes zips with pop ≥ 1000 and no supp. data.
* Denotes zip codes with state prisons.



Based on Spatial Empirical Bayes smoothed point prevalence for week ending 2021-04-17.
Note: New color ramp scale and new ascertainment ratio of 2:1.

Rank	Name	Prev
1	Fredericksburg City	350
2	Lancaster County	340
3	Shenandoah County	320
4	Isle of Wight County	250
5	Warren County	230
6	Floyd County	190
7	Page County	180
8	Manassas City	160
9	Waynesboro City	160
10	New Kent County	150



Note: Scale differs from general public prevalence maps.

Current Hot-Spots

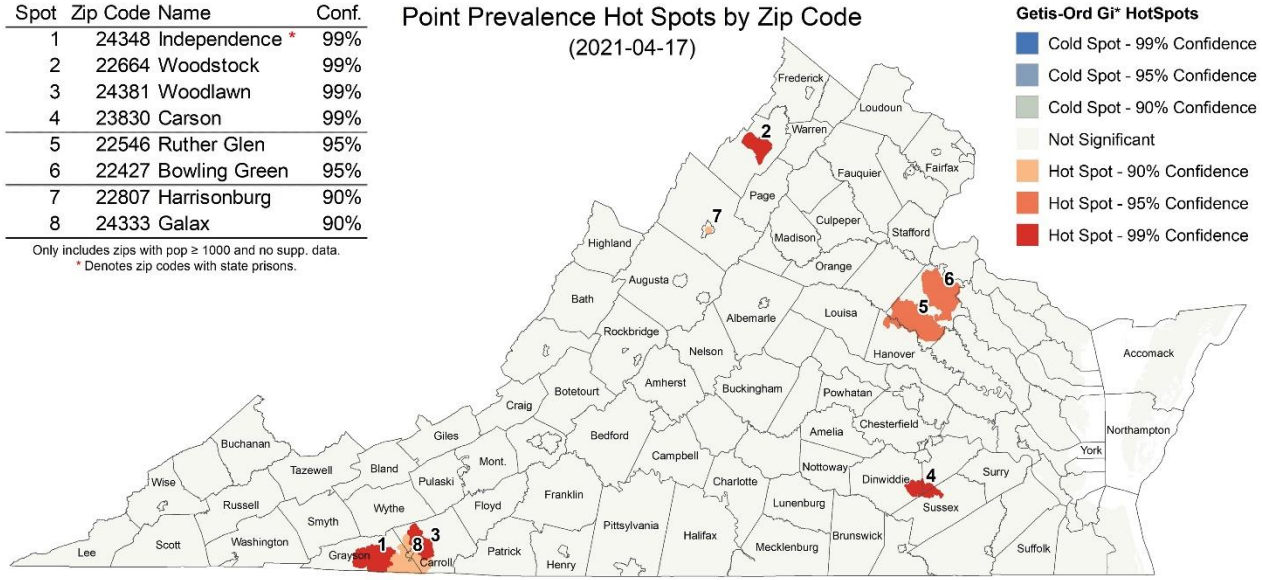
Case rates that are significantly different from neighboring areas or model projections

- **Spatial**: SaTScan based hot spots compare clusters of zip codes with weekly case prevalence higher than nearby zip codes to identify larger areas with statistically significant deviations
- **Temporal**: The weekly case rate (per 100K) projected last week compared to observed by county, which highlights temporal fluctuations that differ from the model's projections

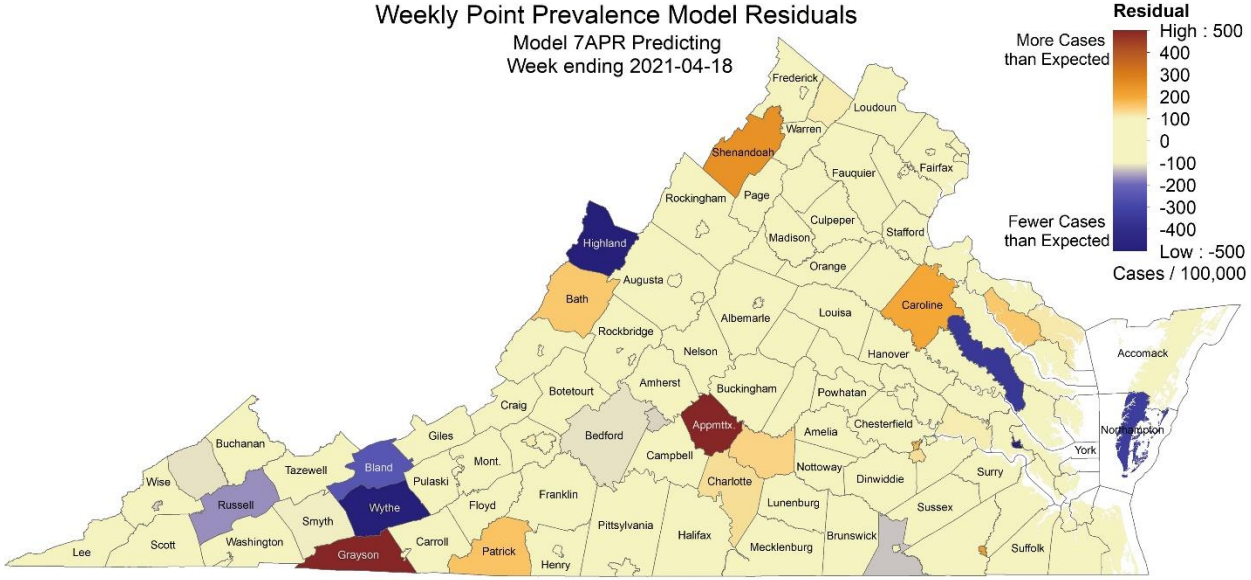
Spatial Hotspots

Spot	Zip Code	Name	Conf.
1	24348	Independence *	99%
2	22664	Woodstock	99%
3	24381	Woodlawn	99%
4	23830	Carson	99%
5	22546	Ruther Glen	95%
6	22427	Bowling Green	95%
7	22807	Harrisonburg	90%
8	24333	Galax	90%

Only includes zips with pop ≥ 1000 and no supp. data.
* Denotes zip codes with state prisons.



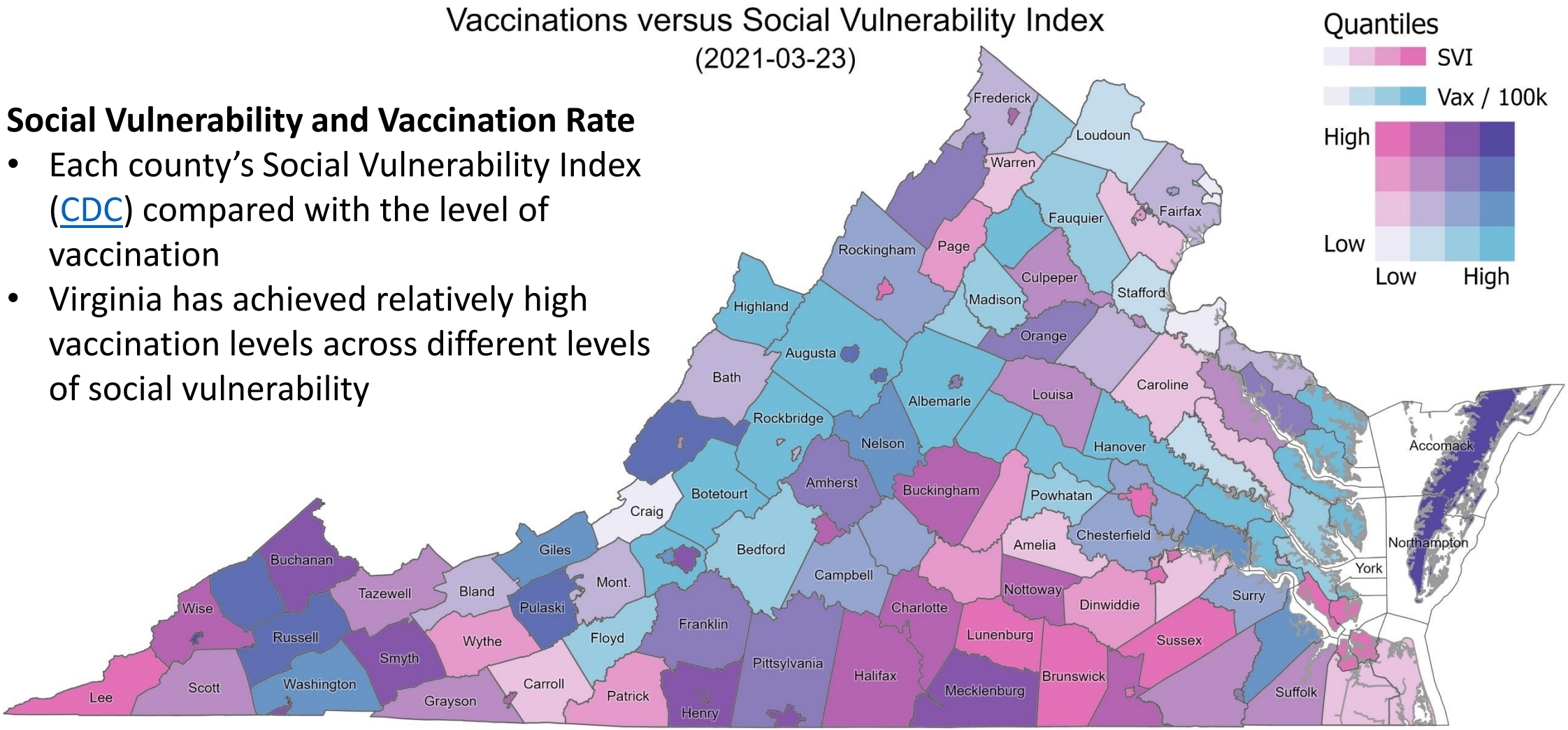
Temporal Hotspots



Social Vulnerability Impact on Vaccination

Social Vulnerability and Vaccination Rate

- Each county's Social Vulnerability Index (CDC) compared with the level of vaccination
- Virginia has achieved relatively high vaccination levels across different levels of social vulnerability



Model Update – Adaptive Fitting

Adaptive Fitting Approach

Each county fit precisely, with recent trends used for future projection

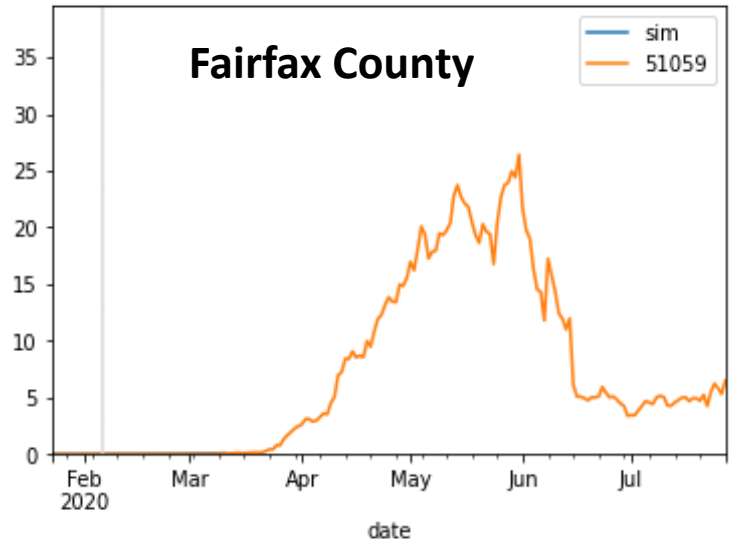
- Allows history to be precisely captured, and used to guide bounds on projections

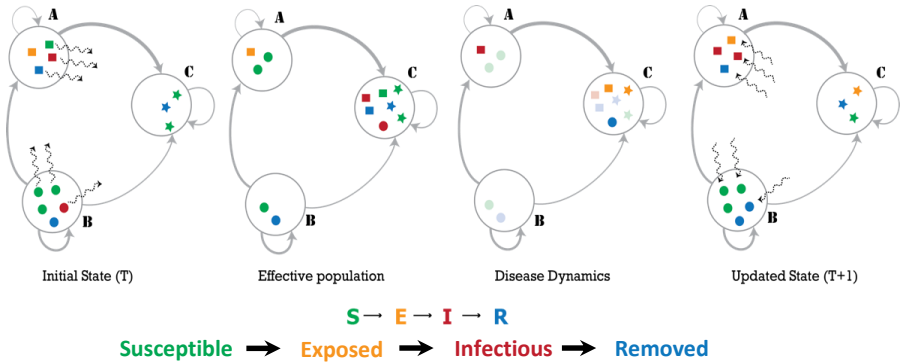
Model: An alternative use of the same meta-population model, PatchSim

- Allows for future "what-if" Scenarios to be layered on top of calibrated model
- Eliminates connectivity between patches, to allow calibration to capture the increasingly unsynchronized epidemic

External Seeding: Steady low-level importation

- Widespread pandemic eliminates sensitivity to initial conditions
- Uses steady 1 case per 10M population per day external seeding





Using Ensemble Model to Guide Projections

Ensemble methodology that combines the Adaptive with machine learning and statistical models such as:

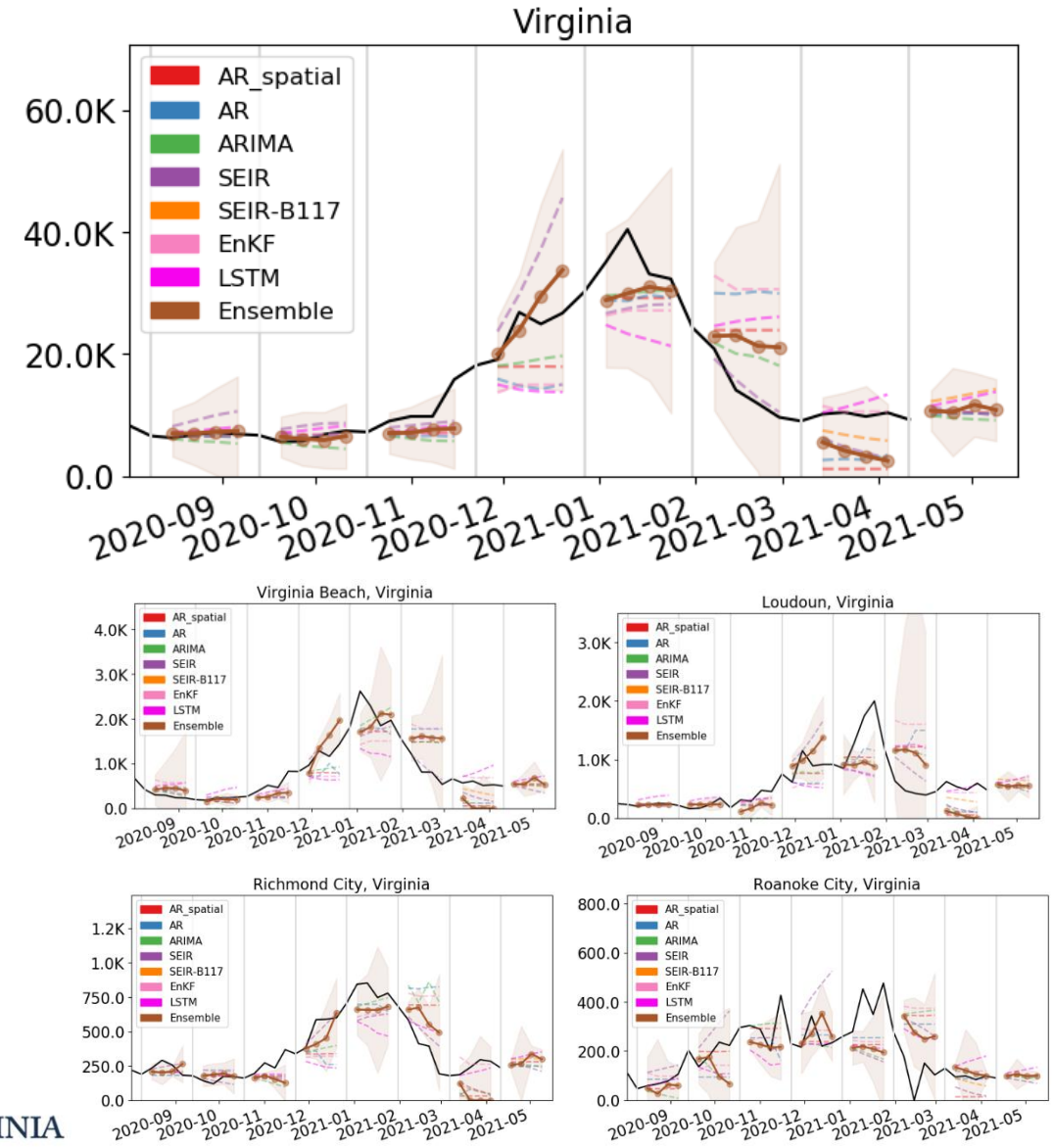
- Autoregressive (AR, ARIMA)
- Neural networks (LSTM)
- Kalman filtering (EnKF)

<u>Weekly forecasts</u> done at county level.

Models chosen because of their track record in disease forecasting and to increase diversity and robustness.

Ensemble forecast provides additional ‘surveillance’ for making scenario-based projections.

Also submitted to CDC Forecast Hub.



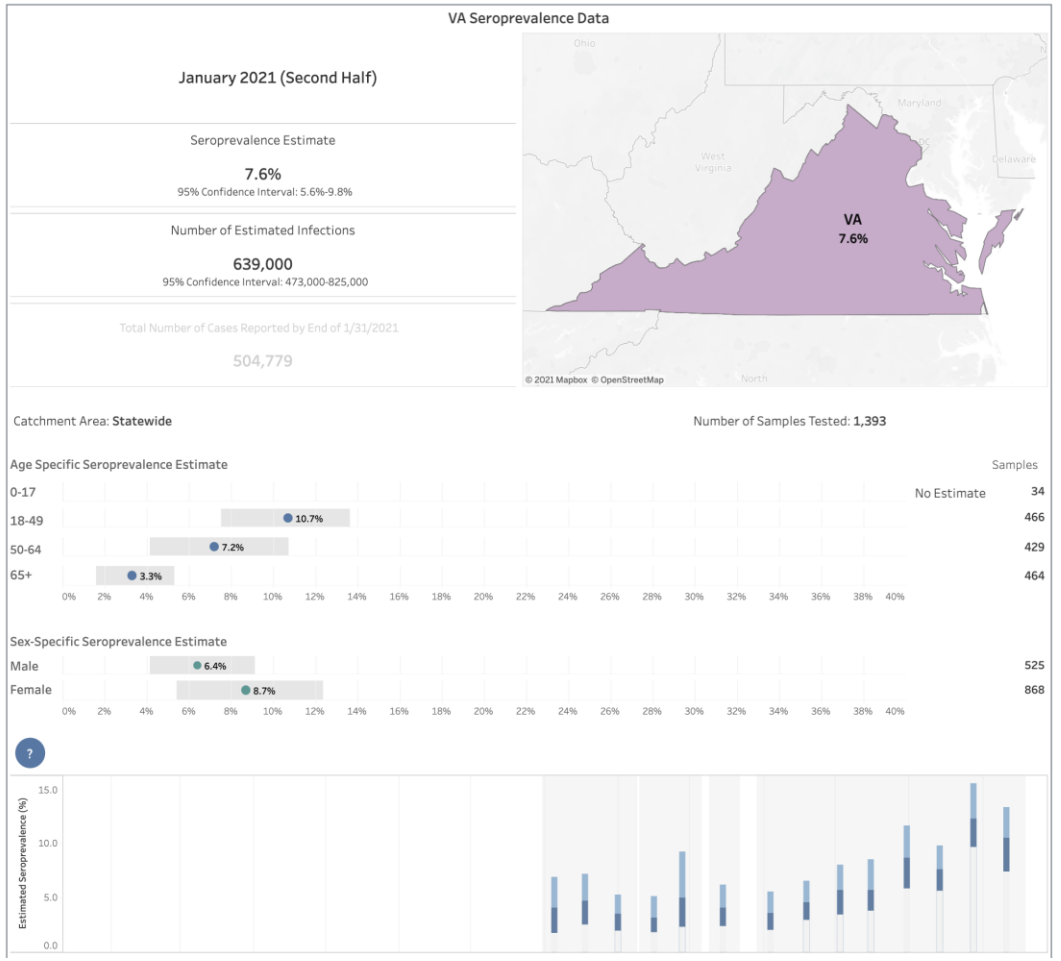
Seroprevalence updates to model design

Several seroprevalence studies provide better picture of how many actual infections have occurred

- CDC Nationwide Commercial Laboratory Seroprevalence Survey estimated 7.6% [5.6% – 9.8%] seroprevalence as of Jan 7th – 21st up from 5.7% a month earlier

These findings are equivalent to an ascertainment ratio of ~2x in the future, with bounds of (1.3x to 3x)

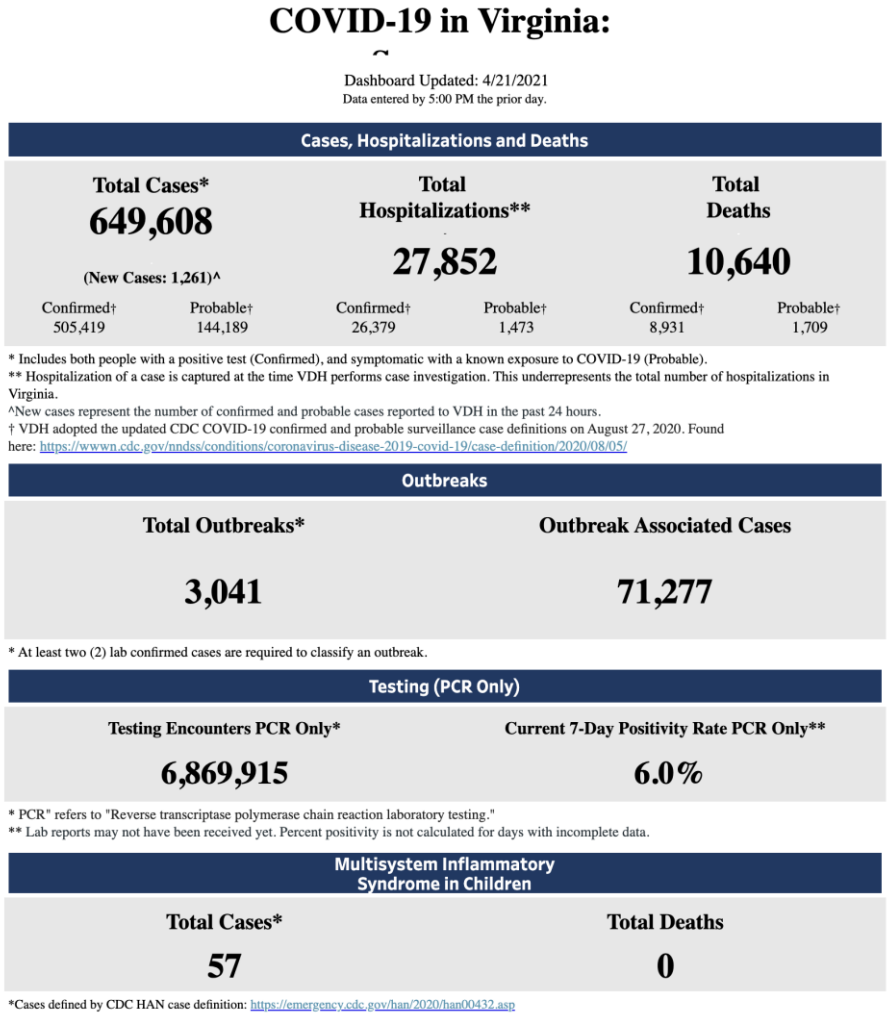
- Thus for 2x there are 2 total infections in the population for every confirmed case recently
- This measure now fully tracks the estimated ascertainment over time
- Uncertainty design has been shifted to these bounds (previously higher ascertainments as was consistent earlier in the pandemic were being used)



https://covid.cdc.gov/covid-data-tracker/#national-lab

Calibration Approach

- **Data:**
  - County level case counts by date of onset (from VDH)
  - Confirmed cases for model fitting
- **Calibration:** fit model to observed data and ensemble's forecast
  - Tune transmissibility across ranges of:
    - Duration of incubation (5-9 days), infectiousness (3-7 days)
    - Undocumented case rate (1x to 7x) guided by seroprevalence studies
    - Detection delay: exposure to confirmation (4-12 days)
  - Approach captures uncertainty, but allows model to precisely track the full trajectory of the outbreak
- **Project:** future cases and outcomes generated using the collection of fit models run into the future
  - **Mean trend from last 7 days of observed cases and first week of ensemble's forecast used**
  - Outliers removed based on variances in the previous 3 weeks
  - 2 week interpolation to smooth transitions in rapidly changing trajectories



COVID-19 in Virginia:

Dashboard Updated: 4/21/2021
Data entered by 5:00 PM the prior day.

Cases, Hospitalizations and Deaths

Total Cases*		Total Hospitalizations**		Total Deaths	
649,608		27,852		10,640	
(New Cases: 1,261)^					
Confirmed†	Probable†	Confirmed†	Probable†	Confirmed†	Probable†
505,419	144,189	26,379	1,473	8,931	1,709

* Includes both people with a positive test (Confirmed), and symptomatic with a known exposure to COVID-19 (Probable).
** Hospitalization of a case is captured at the time VDH performs case investigation. This underrepresents the total number of hospitalizations in Virginia.
^New cases represent the number of confirmed and probable cases reported to VDH in the past 24 hours.
† VDH adopted the updated CDC COVID-19 confirmed and probable surveillance case definitions on August 27, 2020. Found here: https://wwwn.cdc.gov/nndss/conditions/coronavirus-disease-2019-covid-19/case-definition/2020/08/05/

Outbreaks

Total Outbreaks*	Outbreak Associated Cases
3,041	71,277

* At least two (2) lab confirmed cases are required to classify an outbreak.

Testing (PCR Only)

Testing Encounters PCR Only*	Current 7-Day Positivity Rate PCR Only**
6,869,915	6.0%

* PCR" refers to "Reverse transcriptase polymerase chain reaction laboratory testing."
** Lab reports may not have been received yet. Percent positivity is not calculated for days with incomplete data.

Multisystem Inflammatory Syndrome in Children

Total Cases*	Total Deaths
57	0

*Cases defined by CDC HAN case definition: https://emergency.cdc.gov/han/2020/han00432.asp

Accessed 9:00am April 21, 2021

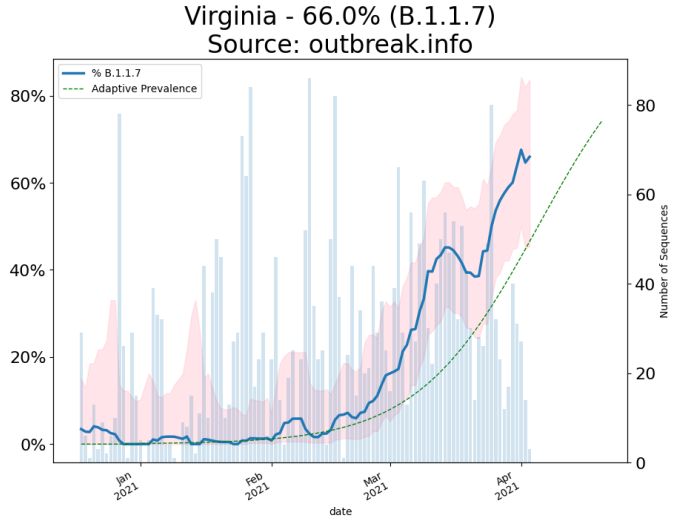
https://www.vdh.virginia.gov/coronavirus/

Scenarios – Transmission Control

- Variety of factors continue to drive transmission rates
  - Seasonal impact of weather patterns, travel and gatherings, fatigue and premature relaxation of infection control practices
- Plausible levels of transmission can be bounded by past experience
  - Assess transmission levels at the county level since May 1, 2020 through present
  - Use the highest and lowest levels experienced (excluding outliers) as plausible bounds for levels of control achievable
  - Transition from current levels of projection to the new levels over 2 months
  - BestPast Control starts with 3 week delay to account for transition to higher levels of control
- Projection Scenario:
  - **BestPast Control:** Lowest level of transmission (5^{th} percentile)
  - **Fatigued Control**: Highest level of transmission (95^{th} percentile) increased by additional 5%

Scenarios – Variant B.1.17

- New Variant B.1.1.7 is best understood and is in Virginia
  - **Transmission increase**: 50% increase from the current baseline projection based on estimated prevalence in past and future
  - **Increased Severity**: 60% increase in likelihood of hospitalization and a 60% increase in mortality Nature
  - **Emergence timing:** Gradual frequency increase reaching 50% frequency on April 5th, a couple weeks after the national estimate in MMWR report from CDC and refined by Andersen et al.
- Variant planning Scenario:
  - **DominantB117**: Current projected transmissibility continues to increase through June to a level 50% more transmissible



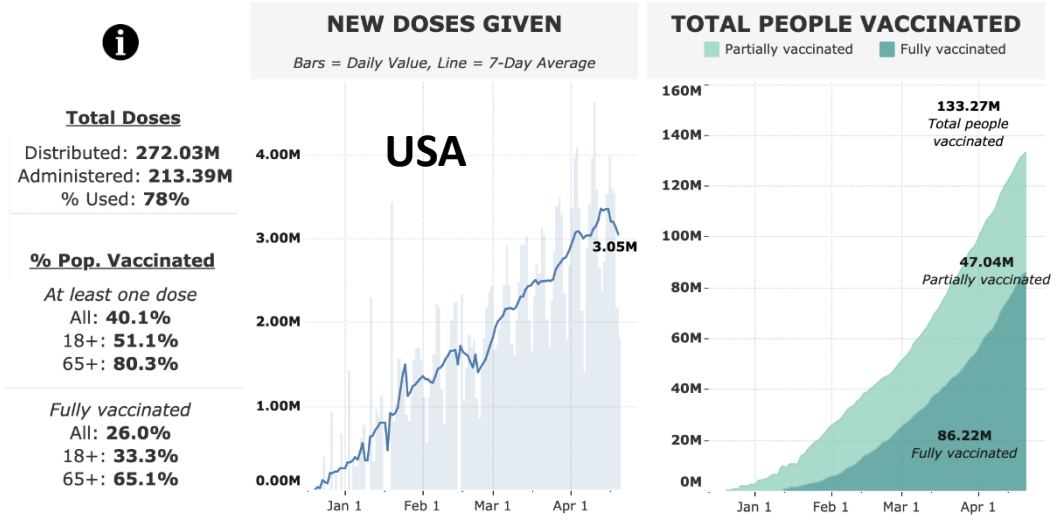
Estimated frequency from public genome repository with added analysis: 66%
Current frequency used in model: 70%

outbreak.info
Outbreak Info

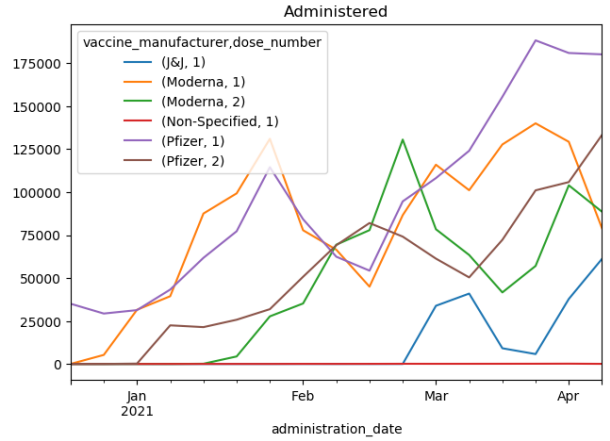
GISAID

Scenarios – Vaccines

- Projected vaccine schedules constructed using current administration rates by dose and manufacturer for VA counties.
- Assumed vaccine efficacies
  - **Pfizer/Moderna**: 50% after first dose, 95% after second dose (3.5 week gap between doses)
  - **J &J** : 67% efficacy after first (and only) dose
  - Delay to efficacy from dose assumed to be 14 days
  - Immunity assumed to last duration of simulation (NEJM study shows long lasting, at least 7 months)
- Pause in J&J administration assumed to continue into the future
- Administration Rate:
  - Pfizer: 158K courses initiated per week
  - Moderna: 79K courses initiated per week
  - J &J: 0 courses initiated per week



Source: https://ckelly17.github.io/vaccine_dashboard.html



VA doses administered by manufacturer

Scenarios – Seasonal Effects and Vaccines

Three scenarios combine these control effects and use the current vaccine schedule

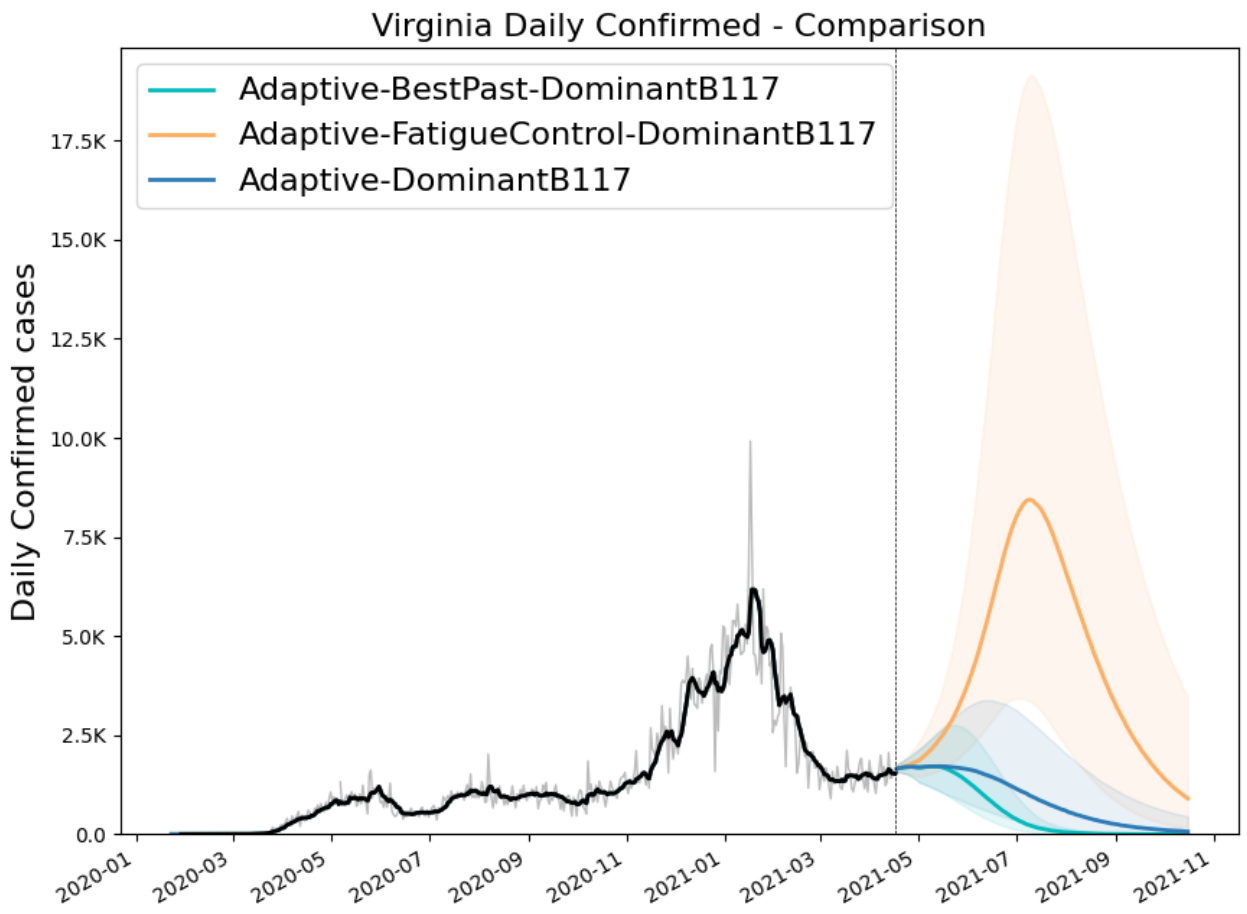
- **Adaptive-DominantB117**: Boosting of transmissibility from the emergence and likely dominance of B.1.1.7
- **Adaptive-BestPast-DominantB117:** Best Past controls with transmission boost from B.1.1.7
- **Adaptive-FatigueControl-DominantB117:** Fatigued controls and transmission boost from B.1.1.7

Counterfactuals with no vaccine (“NoVax”) are provided for comparison purposes

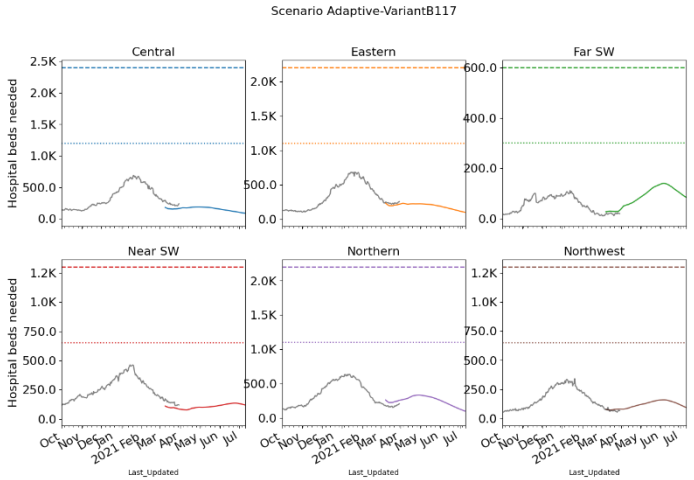
Model Results

Outcome Projections

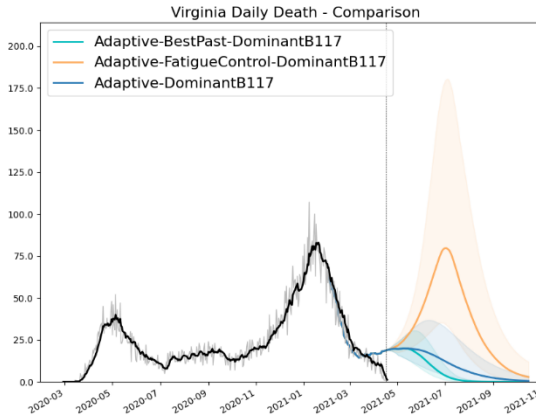
Confirmed cases



Estimated Hospital Occupancy

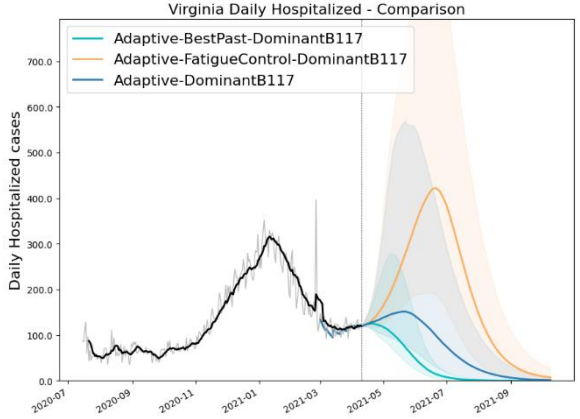


Daily Deaths



Death ground truth from VDH "Event Date" data, most recent dates are not complete

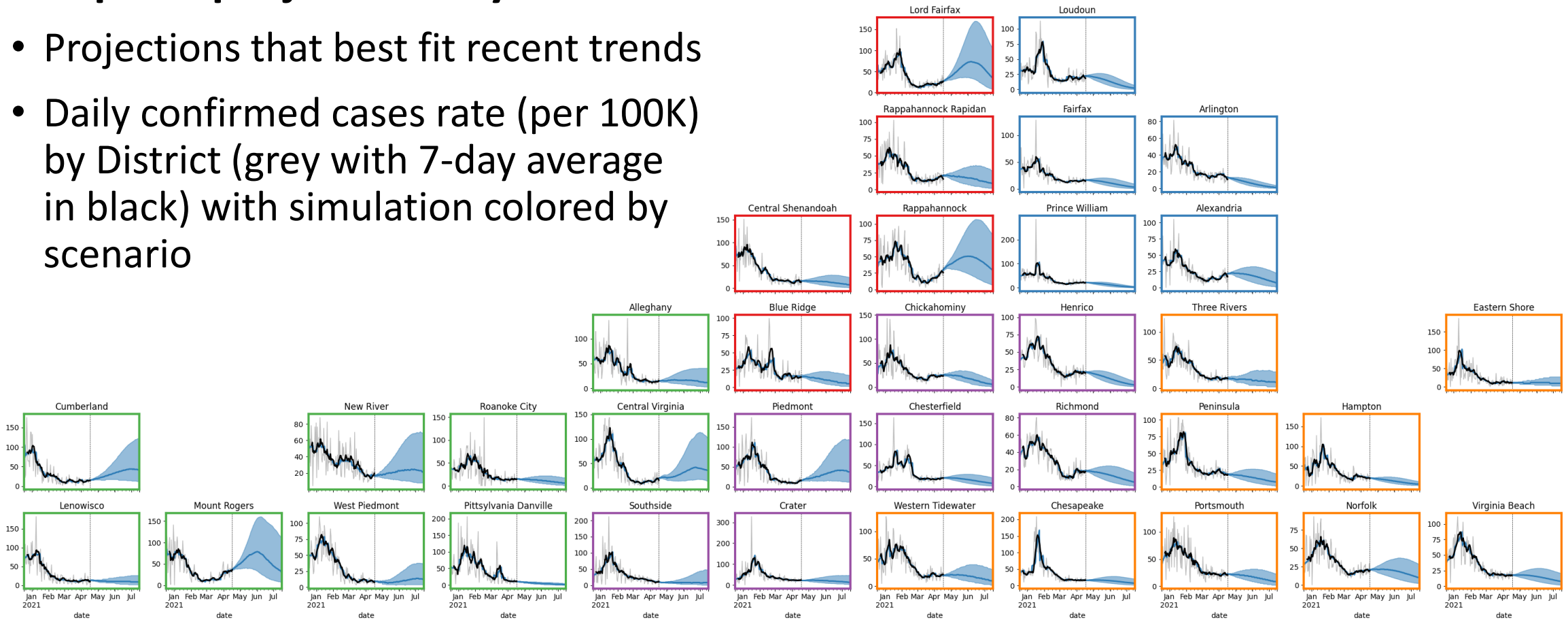
Daily Hospitalized



District Level Projections: Adaptive-DominantB117

Adaptive projections by District

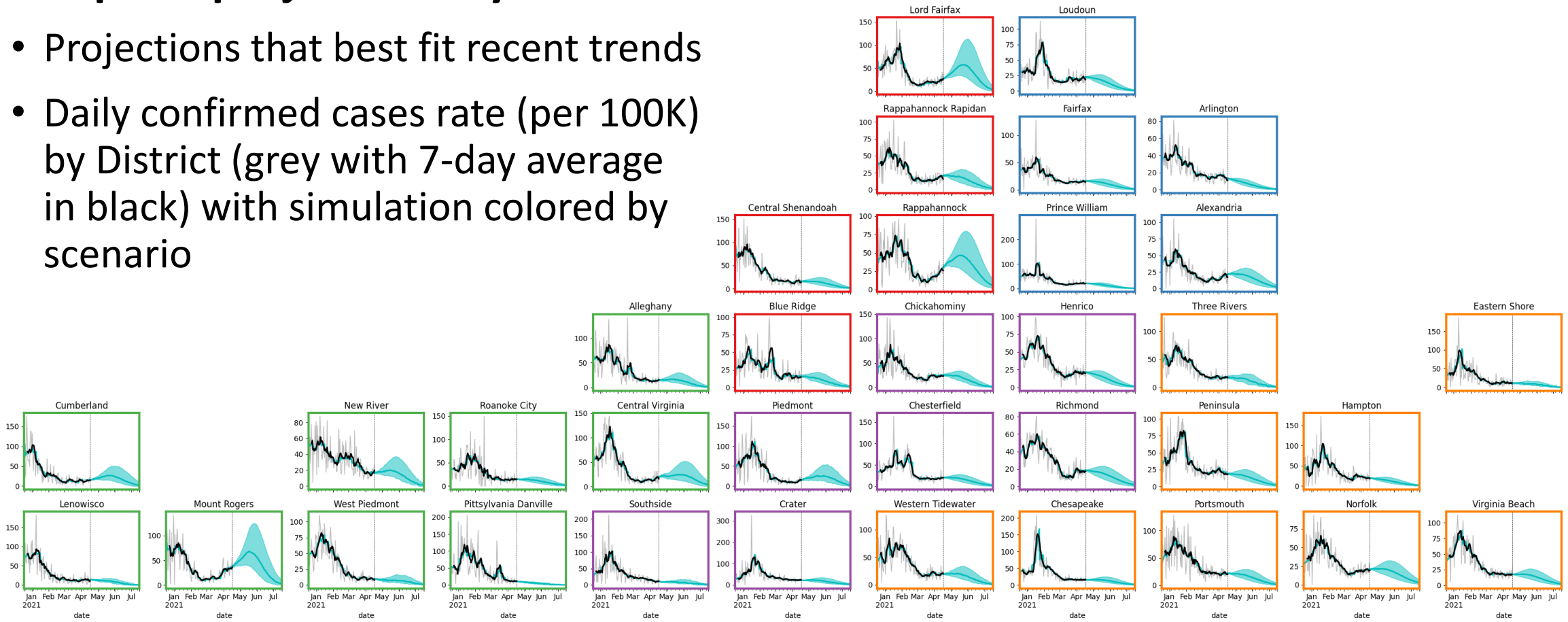
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by District (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-BestPast-DominantB117

Adaptive projections by District

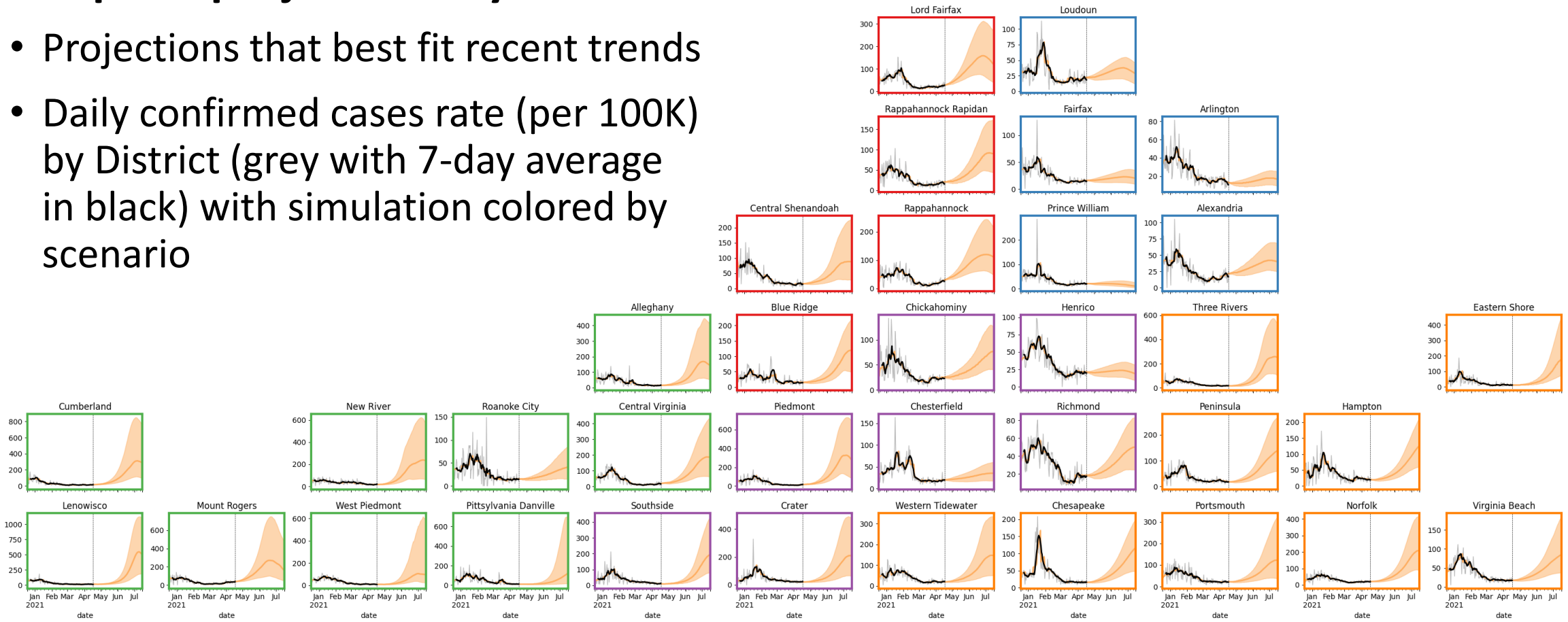
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by District (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-FatigueControl-DominantB117

Adaptive projections by District

- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by District (grey with 7-day average in black) with simulation colored by scenario



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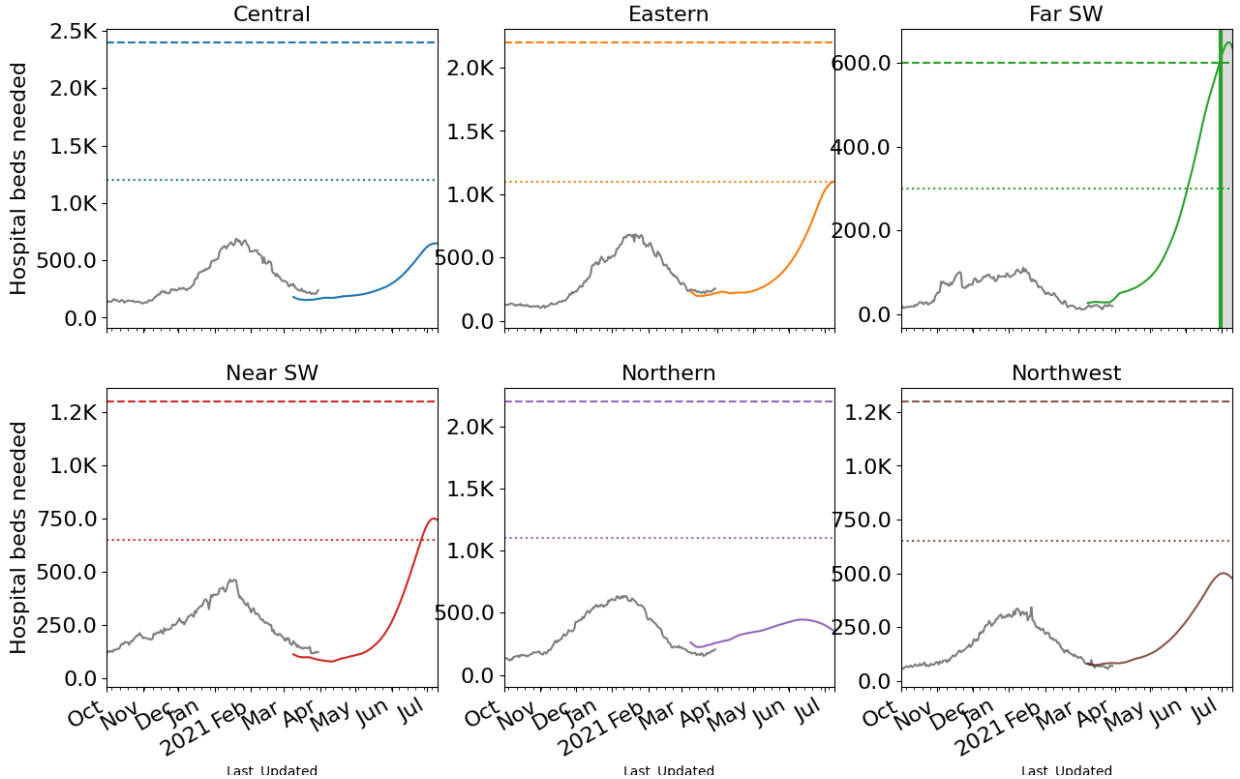
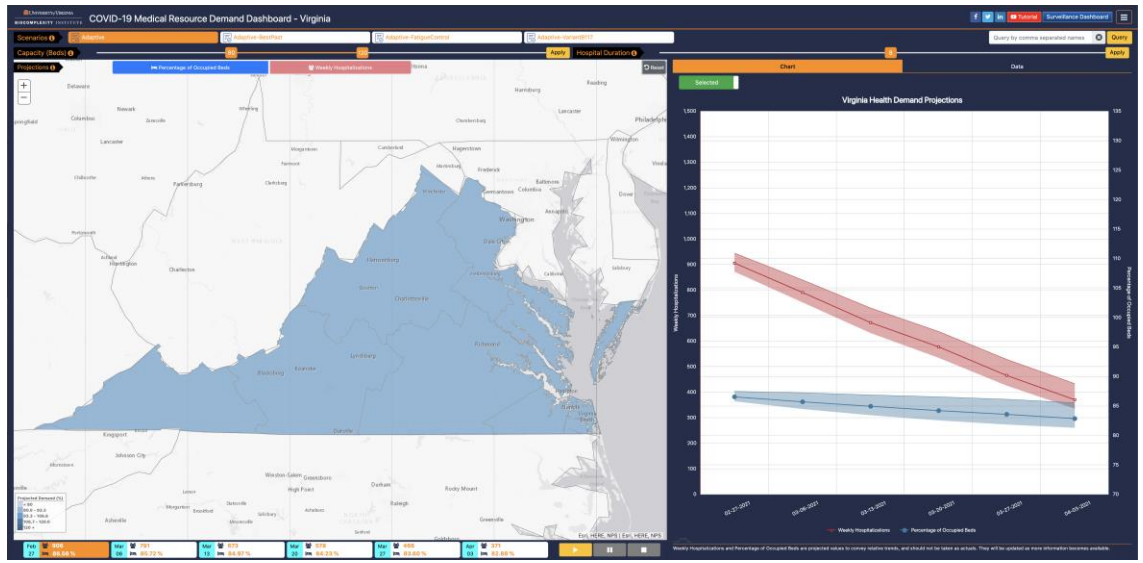
Hospital Demand and Bed Capacity by Region

Capacities* by Region – Adaptive-FatigueControl-DominantB117

COVID-19 capacity ranges from 80% (dots) to 120% (dash) of total beds





https://nssac.bii.virginia.edu/covid-19/vmrddash/

If Adaptive-FatigueControl-DominantB117 scenario:

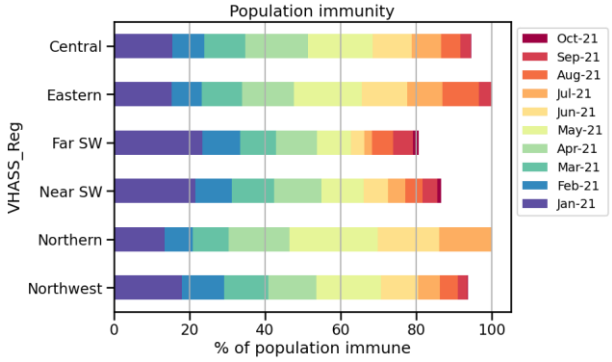
- Southwest initial bed capacity may be approached in early June, with surge capacity approached in July
- Eastern region approaches initial capacity in July

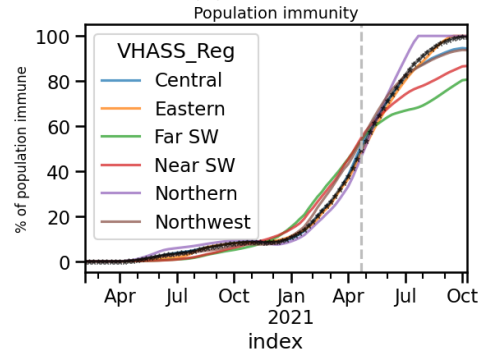
* Assumes average length of stay of 8 days

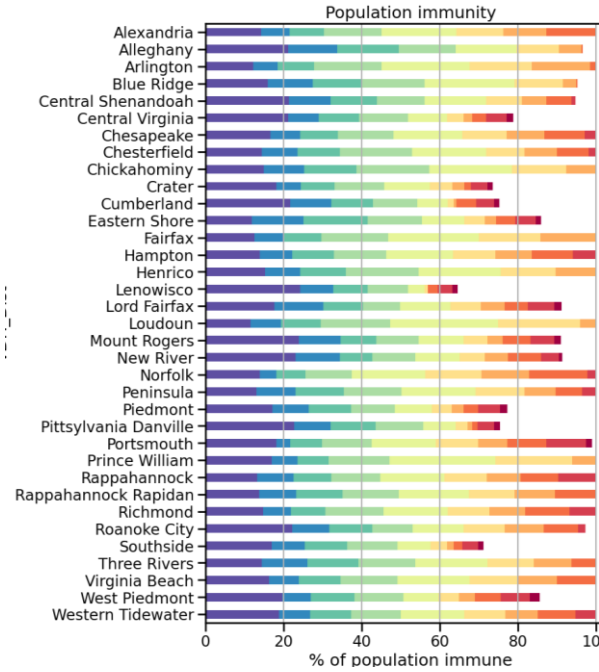
Virginia's Progress on Population Immunity

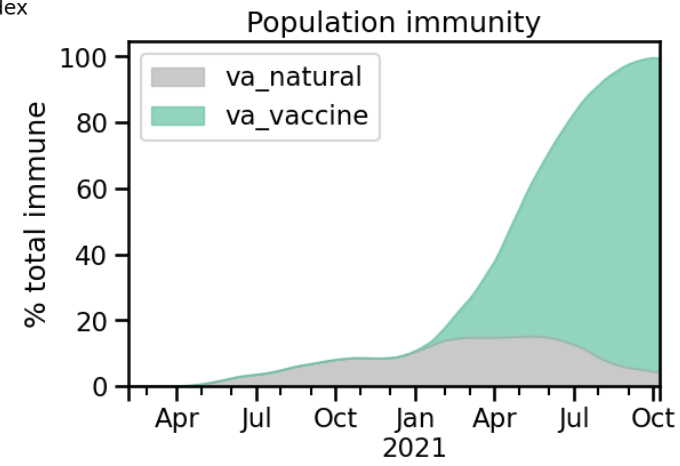
Natural Immunity and Vaccines combine to produce a population level of immunity

- How long immunity from infection with SARS-CoV2 lasts is not well understood but may vary based on severity of symptoms
  - We assume a conservative 6 month period of protection for these calculations
- Vaccine induced immunity is likely to last longer, we assume indefinite protection
  - This also assumes that all administered vaccines remain protective against current and future novel variants
- Population immunity depends on a very high proportion of the population getting vaccinated
  - Using regional vaccine acceptance









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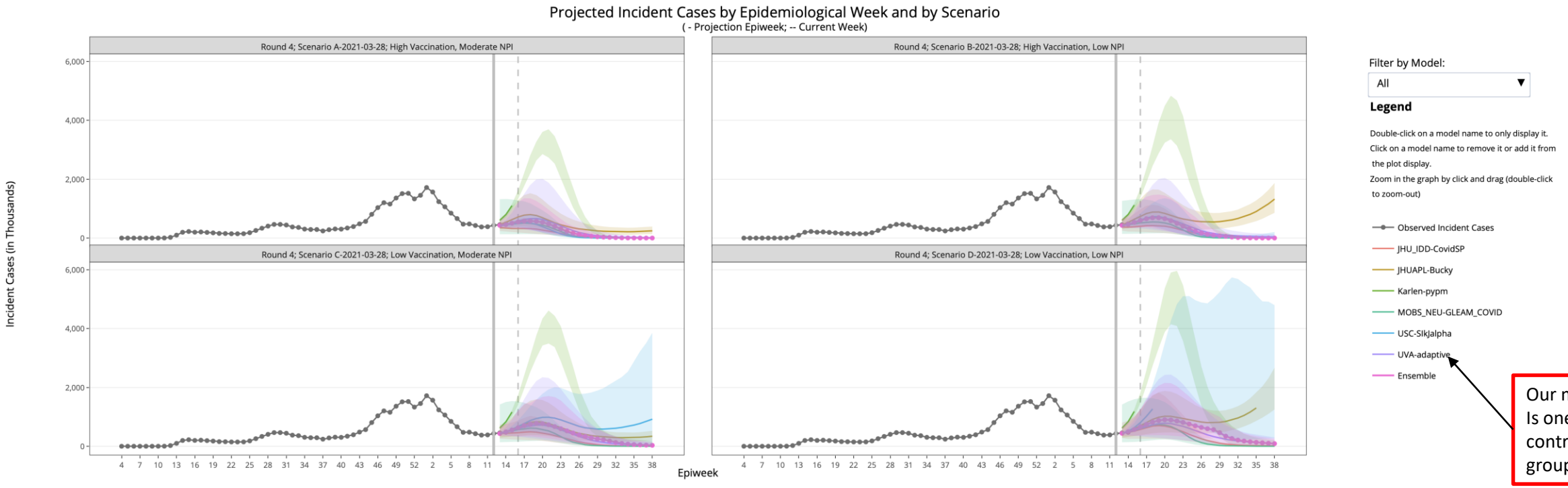
COVID-19 Scenario Modeling Hub

Model Projection

https://covid19scenariomodelinghub.org/viz.html



Collaboration of multiple academic teams to provide national and state-by-state level projections for 4 aligned scenarios that vary vaccine rates (high – low) and levels of control (moderate and low)

- Similar to our current scenarios with variations/updates planned for every 4-5 weeks

Key Takeaways

Projecting future cases precisely is impossible and unnecessary.
Even without perfect projections, we can confidently draw conclusions:

- **Case rates in Virginia have flattened with mix of growth and decline across districts**
- VA mean weekly incidence down to 16/100K from 19/100K, US flat (19 from 19 per 100K)
- Progress remains stalled but is consistent with controls holding their ground despite boosting from B.1.1.7
- Projections show minimal growth overall across Commonwealth, boosted by B.1.1.7, but curtailed by vaccine
- Recent updates:
  - Updated estimates of regional vaccine hesitancy and folded into projections
  - Modeled age-specific vaccinations past and future as well as severity of B.1.1.7 to drive outcome projections
    - Hospitalizations and deaths **reduced** by vaccination in ages most at risk for severe outcomes, but **increased** by prevalence of B.1.1.7
- The situation continues to change. Models continue to be updated regularly.

References

Venkatramanan, S., et al. "Optimizing spatial allocation of seasonal influenza vaccine under temporal constraints." *PLoS Computational Biology* 15.9 (2019): e1007111.

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NSSAC. PatchSim: Code for simulating the metapopulation SEIR model. https://github.com/NSSAC/PatchSim

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Biocomplexity Institute. COVID-19 Surveillance Dashboard. https://nssac.bii.virginia.edu/covid-19/dashboard/

Google. COVID-19 community mobility reports. https://www.google.com/covid19/mobility/

Biocomplexity page for data and other resources related to COVID-19: https://covid19.biocomplexity.virginia.edu/

Questions?

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Supplemental Slides

Weekly Cases and Hospitalizations

Weekly confirmed cases

Week Ending	Adaptive-DominantB117	Adaptive-BestPast-Dominant B117	Adaptive-Fatigued Control -DominantB117
4/18/21	11,041	11,041	11,041
4/25/21	11,767	11,770	11,869
5/2/21	11,851	11,851	12,643
5/9/21	11,889	11,880	14,043
5/16/21	11,986	11,924	16,202
5/23/21	11,893	11,394	19,040
5/30/21	11,693	10,311	22,903
6/6/21	11,348	8,847	27,958
6/13/21	10,744	7,159	34,362
6/20/21	9,997	5,493	41,859
6/27/21	9,103	3,947	49,547
7/4/21	8,093	2,694	55,628

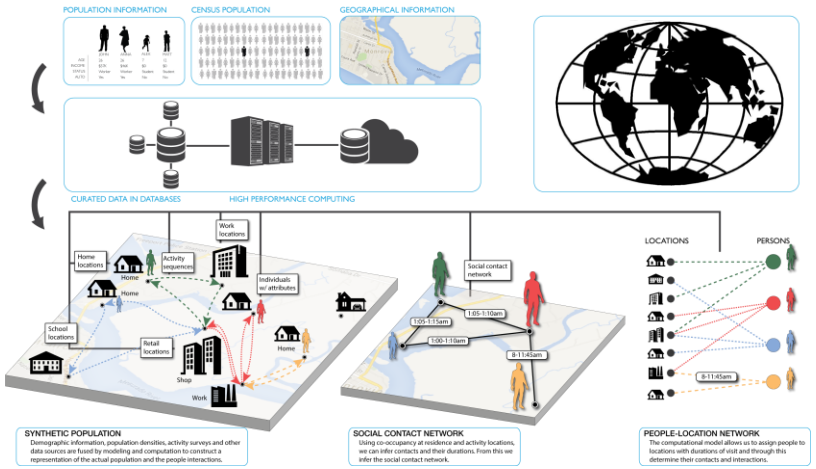
Weekly Hospitalizations

Week Ending	Adaptive-DominantB117	Adaptive-BestPast-Dominant B117	Adaptive-Fatigued Control -DominantB117
4/11/21	865	865	865
4/18/21	906	906	914
4/25/21	921	921	983
5/2/21	925	924	1,094
5/9/21	928	923	1,256
5/16/21	913	874	1,460
5/23/21	887	780	1,731
5/30/21	848	658	2,067
6/6/21	789	522	2,462
6/13/21	720	392	2,885
6/20/21	642	275	3,288
6/27/21	559	182	3,497

Agent-based Model (ABM)

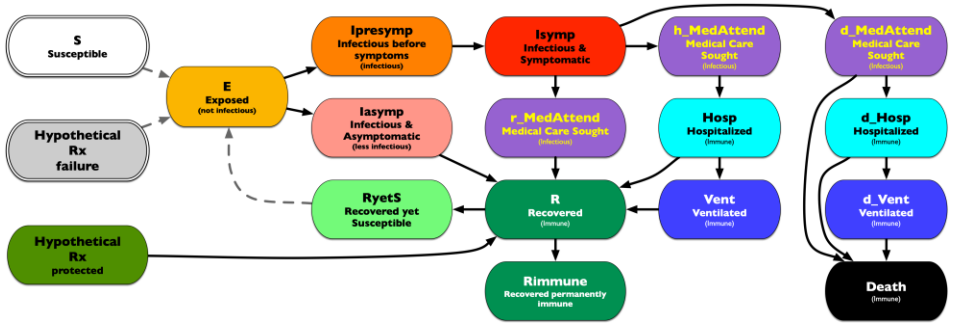
EpiHiper: Distributed network-based stochastic disease transmission simulations

- Assess the impact on transmission under different conditions
- Assess the impacts of contact tracing



Synthetic Population

- Census derived age and household structure
- Time-Use survey driven activities at appropriate locations



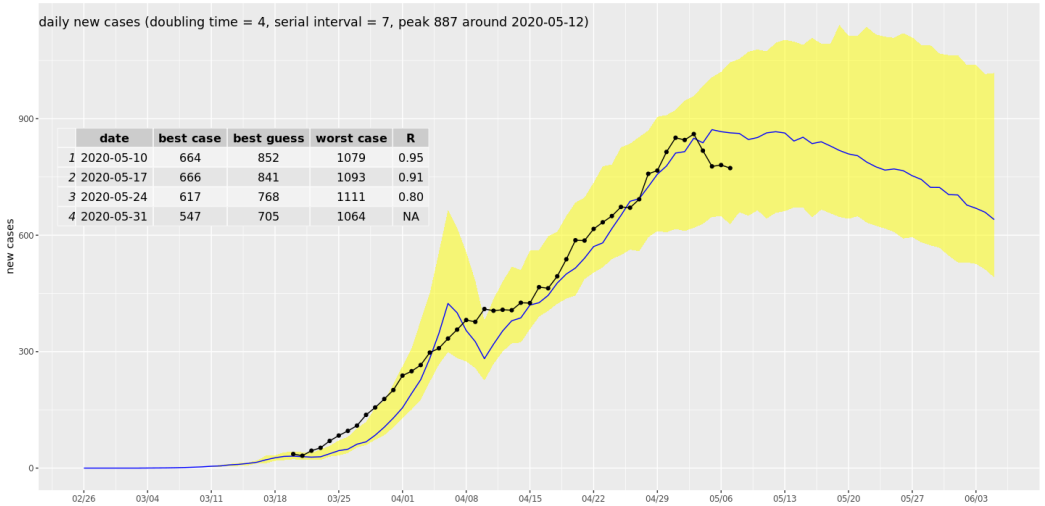
Detailed Disease Course of COVID-19

- Literature based probabilities of outcomes with appropriate delays
- Varying levels of infectiousness
- Hypothetical treatments for future developments

ABM Social Distancing Rebound Study Design

Study of ”Stay Home” policy adherence

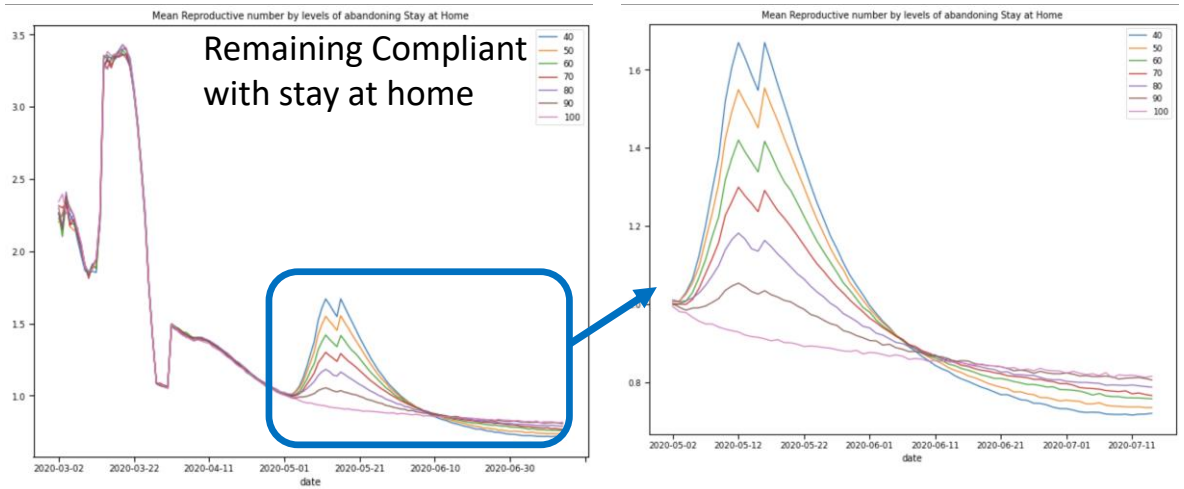
- Calibration to current state in epidemic
- Implement “release” of different proportions of people from ”staying at home”



	date	best case	best guess	worst case	R
1	2020-05-10	664	852	1079	0.95
2	2020-05-17	666	841	1093	0.91
3	2020-05-24	617	768	1111	0.80
4	2020-05-31	547	705	1064	NA

Calibration to Current State

- Adjust transmission and adherence to current policies to current observations
- For Virginia, with same seeding approach as PatchSim



Impacts on Reproductive number with release

- After release, spike in transmission driven by additional interactions at work, retail, and other
- At 25% release (70-80% remain compliant)
- Translates to 15% increase in transmission, which represents a 1/6th return to pre-pandemic levels